

Result No.	Score	Query Match	Length	DB ID	Description	SUMMARIES
1	13	65.0	20	3	US-08-504-538A-12	Sequence 12, Appli
2	13	65.0	20	3	US-08-530-052-12	Sequence 12, Appli
3	13	65.0	20	5	PCT-US95-09307-12	Sequence 12, Appli
4	8	40.0	480	4	US-09-211-11470	Sequence 31470, A
5	6	30.0	135	4	US-09-270-767-31648	Sequence 31648, A
6	6	30.0	135	4	US-09-274-969-16	Sequence 46865, A
7	7	30.0	138	4	US-09-232-991A-322834	Sequence 32834, A
8	6	30.0	154	3	US-09-193-104-26	Sequence 26
9	9	30.0	171	4	US-09-251-991A-26818	Sequence 26818, A
10	6	30.0	277	4	US-09-232-991A-17567	Sequence 17567, A
11	6	30.0	282	4	US-09-247-990-16	Sequence 16, Appli
12	6	30.0	282	4	US-09-724-969-16	Sequence 16, Appli
13	6	30.0	282	4	US-09-724-852-16	Sequence 16, Appli
14	6	30.0	346	5	PCT-US96-11602-2	Sequence 2
15	6	30.0	395	4	US-09-439-039A-7940	Sequence 7940, Ap
16	6	30.0	421	4	US-09-248-799A-20409	Sequence 20409, A
17	6	30.0	478	4	US-09-232-991A-22078	Sequence 22078, A
18	6	30.0	800	4	US-19-251-991A-24635	Sequence 24635, A
19	6	30.0	939	4	US-09-854-845-16	Sequence 16, Appli
20	6	30.0	954	4	US-09-854-845-14	Sequence 14, Appli
21	6	30.0	1044	4	US-09-854-845-6	Sequence 6, Appli
22	6	30.0	1049	4	US-09-854-845-2	Sequence 2, Appli
23	6	30.0	1078	4	US-09-854-845-8	Sequence 8, Appli
24	6	30.0	1093	4	US-09-854-845-4	Sequence 4, Appli
25	6	30.0	1136	4	US-09-854-845-12	Sequence 12, Appli
26	6	30.0	1151	4	US-09-854-845-10	Sequence 10, Appli
27	6	30.0	1509	4	US-09-676-519-27	Sequence 27, Appli
28	5	25.0	19	1	US-08-988-024C-7	Sequence 7, Appli
29	5	25.0	19	5	PCT-US93-08214-21	Sequence 21, Appli
30	5	25.0	20	4	US-09-155-613A-6	Sequence 6, Appli
31	5	25.0	20	4	US-09-498-134A-3	Sequence 3, Appli
32	5	25.0	21	1	US-07-944-143C-20	Sequence 20, Appli
33	5	25.0	21	5	PCT-US93-08214-20	Sequence 20, Appli
34	5	25.0	24	1	US-09-155-613A-97	Sequence 97, Appli
35	5	25.0	25	4	US-09-155-613A-1	Sequence 1, Appli
36	5	25.0	25	4	US-09-155-613A-1	Sequence 1, Appli
37	5	25.0	25	4	US-09-155-613A-98	Sequence 98, Appli
38	5	25.0	25	4	US-09-155-613A-22	Sequence 22, Appli
39	5	25.0	35	4	US-09-155-613A-23	Sequence 23, Appli
40	5	25.0	38	1	US-08-179-632-7	Sequence 7, Appli
41	5	25.0	38	5	PCT-US95-00062-7	Sequence 7, Appli
42	5	25.0	38	5	PCT-US95-00062-7	Sequence 7, Appli
43	5	25.0	51	4	US-09-621-976-4432	Sequence 432, Appli
44	5	25.0	60	5	PCT-US94-14074-1	Sequence 1, Appli
45	5	25.0	61	3	US-09-134-001C-3836	Sequence 3836, Appli
46	5	25.0	62	4	US-09-511-999C-4436	Sequence 4436, Appli
47	5	25.0	73	4	US-09-252-991A-29973	Sequence 29973, A
48	5	25.0	76	4	US-09-513-999C-6143	Sequence 6143, Appli
49	5	25.0	79	4	US-09-138-4524-1187	Sequence 1187, Appli
50	5	25.0	79	4	US-09-270-767-59078	Sequence 59078, A
51	5	25.0	82	4	US-09-205-258-403	Sequence 403, Appli
52	5	25.0	88	4	US-09-621-976-3972	Sequence 3972, A
53	5	25.0	92	4	US-09-673-809-25	Sequence 25, Appli
54	5	25.0	98	4	US-09-632-345-4	Sequence 4, Appli
55	5	25.0	98	4	US-09-540-236-2144	Sequence 2144, Appli
56	5	25.0	108	4	US-09-710-279-1724	Sequence 1724, Appli
57	5	25.0	113	4	US-09-621-976-7483	Sequence 7483, Appli
58	5	25.0	119	4	US-09-621-976-5186	Sequence 5186, Appli
59	5	25.0	119	4	US-09-631-976-5890	Sequence 5890, Appli
60	5	25.0	119	4	US-09-513-999C-5792	Sequence 5792, Appli
61	5	25.0	123	4	US-09-816-248-2	Sequence 2, Appli
62	5	25.0	123	4	US-09-816-248-3	Sequence 3, Appli
63	5	25.0	123	4	US-09-816-248-4	Sequence 4, Appli
64	5	25.0	129	3	US-0-980-523-11	Sequence 11, Appli
65	5	25.0	131	4	US-0-950-236-3251	Sequence 3251, Appli
66	5	25.0	137	3	US-0-956-574-4	Sequence 4, Appli
67	5	25.0	137	4	US-08-44-294A-4	Sequence 4, Appli
68	5	25.0	144	4	US-09-210-767-32070	Sequence 32070, A
69	5	25.0	144	4	US-09-210-767-47237	Sequence 47237, A
70	5	25.0	158	4	US-09-223-991A-27339	Sequence 27339, A
71	5	25.0	168	4	US-09-22-991A-20164	Sequence 20164, A
72	5	25.0	168	4	US-09-22-991A-30088	Sequence 30088, A
73	5	25.0	169	4	US-09-222-991A-32088	Sequence 32088, A
74	5	25.0	170	4	US-09-22-991A-18779	Sequence 18779, A
75	5	25.0	173	4	US-09-222-991A-20339	Sequence 20339, A
76	5	25.0	176	4	US-09-252-991A-24481	Sequence 24481, A
77	5	25.0	180	1	US-09-248-798A-17721	Sequence 17721, A
78	5	25.0	182	1	US-08-127-954-135	Sequence 135, Appli
79	5	25.0	182	1	US-08-127-954-137	Sequence 137, Appli
80	5	25.0	182	1	US-08-127-954-138	Sequence 138, Appli
81	5	25.0	182	1	US-08-127-954-139	Sequence 139, Appli
82	5	25.0	182	1	US-08-127-954-140	Sequence 140, Appli
83	5	25.0	182	1	US-08-127-954-141	Sequence 141, Appli
84	5	25.0	182	1	US-08-127-954-142	Sequence 142, Appli
85	5	25.0	182	1	US-08-127-954-143	Sequence 143, Appli
86	5	25.0	182	1	US-08-127-954-144	Sequence 144, Appli
87	5	25.0	182	1	US-08-127-954-145	Sequence 145, Appli
88	5	25.0	182	1	US-08-127-954-146	Sequence 146, Appli
89	5	25.0	182	1	US-08-127-954-147	Sequence 147, Appli
90	5	25.0	182	1	US-08-127-954-148	Sequence 148, Appli
91	5	25.0	182	1	US-08-127-954-149	Sequence 149, Appli
92	5	25.0	182	1	US-08-127-954-153	Sequence 153, Appli
93	5	25.0	182	1	US-08-127-954-154	Sequence 154, Appli
94	5	25.0	182	1	US-08-127-954-155	Sequence 155, Appli
95	5	25.0	182	1	US-08-127-954-156	Sequence 156, Appli
96	5	25.0	182	1	US-08-127-954-157	Sequence 157, Appli
97	5	25.0	182	1	US-08-127-954-158	Sequence 158, Appli
98	5	25.0	182	1	US-08-127-954-159	Sequence 159, Appli
99	5	25.0	182	1	US-08-127-954-160	Sequence 160, Appli
100	5	25.0	182	1	US-08-127-954-161	Sequence 161, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID Description

Result No. Score

RESULT 1
US-08-504-538A-12
Sequence 12, Application US/08504538A

GENERAL INFORMATION:
Patent No.: 6007746
APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN INTERACTIONS

NUMBER OF SEQUENCES: 21
COUNTRY: USA
ZIP: 02110-2214
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/504,538A
FILING DATE: 07/20/95
CLASSIFICATION:
APPLICATION NUMBER: 08/278, 082
FILING DATE: 07/20/94
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REFERENCE/DOCKET NUMBER: 30_162
SEQUENCE/SEQUENCE NUMBER: 00786/259001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: amino acid
STRANDEDNESS: linear

Query Match Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WALGWRWLRYYGW 18
Db 6 WALGWRWLRYYGW 18

RESULT 3
PCT-US95-09307-12
Sequence 12, Application PC/TUS9509307
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jessen, Timm H.
APPLICANT: Xu, Chanxing Wilson
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN INTERACTIONS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09307
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 30,162
 RECOMMUNICATION NUMBER: 007866/2880001
 TELEPHONE: (617) 542-5070
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 PCT-US95-09307-12

Query Match 65.0%; Score 13; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WALGWRWLRGGW 18
 Db 6 WALGWRWLRGGW 18

RESULT 4
 US-09-252-991A-31470
 ; Sequence 31470, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; LENGTH: 480
 ; TYPE: PRT; Organism: Pseudomonas aeruginosa
 ; ORGANISM: Pseudomonas aeruginosa

Query Match 40.0%; Score 8; DB 4; Length 480;
 Best Local Similarity 100.0%; Pred. No. 0.4%;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LGWRWLR 15
 Db 255 LGWRWLR 262

RESULT 5
 US-09-270-767-11648
 ; Sequence 31648, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Bomberger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; CURRENT APPLICATION NUMBER: US/09-066-965a-2
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; LENGTH: 135

Query Match 30.0%; Score 6; DB 4; Length 135;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 WRWLRR 15
 Db 24 WRWLRR 29

RESULT 6
 US-09-270-767-46865
 ; Sequence 46865, Application US/09270767
 ; GENERAL INFORMATION:
 ; APPLICANT: Bomberger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-94
 ; CURRENT APPLICATION NUMBER: US/09-270-767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 46865
 ; LENGTH: 135

Query Match 30.0%; Score 6; DB 4; Length 135;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 WRWLRR 15
 Db 24 WRWLRR 29

RESULT 7
 US-09-252-991A-32834
 ; Sequence 32834, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 32834
 ; LENGTH: 138

Query Match 30.0%; Score 6; DB 4; Length 138;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 WRWLRR 15
 Db 49 WRWLRR 54

RESULT 8
 US-09-193-104-26

Sequence 26, Application US/09193104A
 Patent No. 6172293
 GENERAL INFORMATION:
 APPLICANT: Prim, Daniele
 APPLICANT: Fiordalisi, Gianfranco
 APPLICANT: Palla, Mario
 TITLE OF INVENTION: Escape Mutant of the Surface Antigen of Hepatitis B
 TITLE OF INVENTION: Virus
 FILE REFERENCE: SBD110467
 CURRENT APPLICATION NUMBER: US/09/133,104A
 CURRENT FILING DATE: 1998-11-16
 EARLIER APPLICATION NUMBER: EP 97830635.5
 EARLIER FILING DATE: 1997-12-01
 NUMBER OF SEQ ID NOS: 44
 SEQ ID NO: 26
 LENGTH: 154
 TYPE: PRT
 ORGANISM: Hepatitis B virus
 US-09-193-104-26

RESULT 9
 US-09-252-991A-26818
 Sequence 26818, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 26818
 LENGTH: 171
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-26818

Query Match 30.0%; Score 6; DB 3; Length 154;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSWALG 9
 Db 121 SSWALG 126

RESULT 10
 US-09-252-991A-17567
 Sequence 17567, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-10
 PRIOR APPLICATION NUMBER: US 60/105,509

Query Match 30.0%; Score 6; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 WRWLRR 15
 Db 8 WRWLRR 13

RESULT 11
 US-09-247-890-16
 Sequence 16, Application US/09247890
 Patent No. 6541011
 GENERAL INFORMATION:
 APPLICANT: Punnonen, Juha
 APPLICANT: Bass, Steven H.
 APPLICANT: Whalen, Robert Gerald
 APPLICANT: Howard, Russell
 APPLICANT: Stemmer, Willem P.C.
 TITLE OF INVENTION: Antigen Library Immunization
 FILE REFERENCE: 018097-028710US
 CURRENT APPLICATION NUMBER: US/09/247,890
 CURRENT FILING DATE: 1999-02-10
 EARLIER APPLICATION NUMBER: US 60/074,294
 EARLIER FILING DATE: 1998-02-11
 EARLIER APPLICATION NUMBER: US 60/105,509
 EARLIER FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 16
 LENGTH: 282
 TYPE: PRT
 ORGANISM: Woodchuck hepatitis B virus
 US-09-247-890-16

Query Match 30.0%; Score 6; DB 4; Length 282;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSWALG 9
 Db 210 SSWALG 215

RESULT 12
 US-09-724-969-16
 Sequence 16, Application US/09724969
 Patent No. 6561435
 GENERAL INFORMATION:
 APPLICANT: Punnonen, Juha
 APPLICANT: Bass, Steven H.
 APPLICANT: Whalen, Robert Gerald
 APPLICANT: Howard, Russell
 APPLICANT: Stemmer, Willem P.C.
 TITLE OF INVENTION: Antigen Library Immunization
 FILE REFERENCE: 018097-028710US
 CURRENT APPLICATION NUMBER: US/09/724,969
 CURRENT FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: 09/247,890
 PRIOR FILING DATE: 1999-02-10
 PRIOR APPLICATION NUMBER: US 60/105,509

Query Match 30.0%; Score 6; DB 4; Length 171;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSWALG 9
 Db 210 SSWALG 215

OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: PCT/US96/10602
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,814
; FILING DATE: 20-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/2B2001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10602-2

Query Match Score 6; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 4 SSWALG 9
Db 210 SSWALG 215

RESULT 13
US-09-724-852-16
; Sequence 16, Application US/09724852
; Paten. No. 6576757
; GENERAL INFORMATION:
; APPLICANT: Punningen, Juha
; APPLICANT: Bass, Steven H.
; APPLICANT: Whalen, Robert Gerald
; APPLICANT: Howard, Russell
; APPLICANT: Stammer, Willem P.C.
; APPLICANT: Maxygen, Inc.
; TITLE OF INVENTION: Antigen Library Immunization
; CURRENT APPLICATION NUMBER: US/09/724,852
; PRIORITY NUMBER: US/09/247,890
; PRIOR APPLICATION NUMBER: US/09/247,890
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Woodchuck hepatitis B virus
US-09-724-852-16

Query Match Score 6; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 4 SSWALG 9
Db 210 SSWALG 215

RESULT 14
PCT-US96-10602-2
; Sequence 2, Application PCT/US9610602
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

RESULT 15
US-09-489-039A-794C
; Sequence 7940, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709/2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7940
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7940

Query Match Score 6; DB 4; Length 395;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 12 WLRRYG 17
Db 388 WLRRYG 393

RESULT 16
US-09-248-796A-20409
; Sequence 20409, Application US/09248796A
; Parent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107156.132

CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIORITY NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIORITY NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO: 20409
 LENGTH: 421
 TYPE: PRT
 ORGANISM: Candida albicans

US-09-248-796A-20409

Query Match 30.0%; Score 6; DB 4; Length 421;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 7 ALGWRW 12
 Db 129 ALGWRW 134

RESULT 19
 US-09-252-991A-24635
 / Sequence 2078, Application US/09252991A.
 / GENERAL INFORMATION:
 / APPLICANT: Marc J. Rubenfield et al.
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 / FILE REFERENCE: 107196.136
 / CURRENT FILING DATE: 1999-02-18
 / PRIORITY NUMBER: US/09/252,991A
 / PRIOR FILING DATE: 1998-02-18
 / PRIORITY NUMBER: US 60/094,190
 / PRIOR FILING DATE: 1998-07-27
 / NUMBER OF SEQ ID NOS: 33142
 / SEQ ID NO: 22078
 / LENGTH: 478
 / TYPE: PRT
 / ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22078

Query Match 30.0%; Score 6; DB 4; Length 478;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 WRWIRR 15
 Db 443 WRWIRR 448

RESULT 18
 US-09-252-991A-24635
 / Sequence 24635, Application US/09252991A.
 / GENERAL INFORMATION:
 / APPLICANT: Marc J. Rubenfield et al.
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 / TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 / FILE REFERENCE: 107196.136
 / CURRENT FILING DATE: 1999-02-18
 / PRIORITY NUMBER: US/09/252,991A
 / PRIOR FILING DATE: 1998-02-18
 / PRIORITY NUMBER: US 60/094,190
 / PRIOR FILING DATE: 1998-07-27
 / NUMBER OF SEQ ID NOS: 33142
 / SEQ ID NO: 24635
 / LENGTH: 800
 / TYPE: PRT
 / ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-24635

Query Match 30.0%; Score 6; DB 4; Length 800;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 WRWIRR 15
 Db 487 WRWIRR 492

RESULT 19
 US-09-854-845-16
 / Sequence 16, Application US/09854845
 / Patent No. 6750054
 / GENERAL INFORMATION:
 / APPLICANT: Walk, D. Wade
 / APPLICANT: Wang, Xiaoming
 / APPLICANT: Scoville, John
 / APPLICANT: Turner, C. Alexander Jr.
 / TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
 / FILE REFERENCE: LEX-0177-USA
 / CURRENT APPLICATION NUMBER: US/09/854,845
 / CURRENT FILING DATE: 2001-05-14
 / PRIOR APPLICATION NUMBER: US 60/205,274
 / PRIOR FILING DATE: 2000-05-18
 / PRIOR APPLICATION NUMBER: US 60/208,893
 / PRIOR FILING DATE: 2000-06-02
 / NUMBER OF SEQ ID NOS: 50
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 16
 / LENGTH: 939
 / TYPE: PRT
 / ORGANISM: homo sapiens

US-09-854-845-16

Query Match 30.0%; Score 6; DB 4; Length 939;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 3 WSSWAL 8
 Db 473 WSSWAL 478

RESULT 20
 US-09-854-845-14
 / Sequence 14, Application US/09854845
 / Patent No. 6750054
 / GENERAL INFORMATION:
 / APPLICANT: Walk, D. Wade
 / APPLICANT: Wang, Xiaoming
 / APPLICANT: Scoville, John
 / APPLICANT: Turner, C. Alexander Jr.
 / TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
 / FILE REFERENCE: LEX-0177-USA
 / CURRENT APPLICATION NUMBER: US/09/854,845
 / CURRENT FILING DATE: 2001-05-14
 / PRIOR APPLICATION NUMBER: US 60/205,274
 / PRIOR FILING DATE: 2000-05-18
 / PRIOR APPLICATION NUMBER: US 60/208,893
 / PRIOR FILING DATE: 2000-06-02
 / NUMBER OF SEQ ID NOS: 50
 / SOFTWARE: FastSEQ for Windows Version 4.0
 / SEQ ID NO: 14
 / LENGTH: 954
 / TYPE: PRT
 / ORGANISM: homo sapiens

US-09-854-845-14

Query Match 30.0%; Score 6; DB 4; Length 954;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 3 WSSWAL 8
Db 473 WSSWAL 478

RESULT 21
US-09-854-845-6
; Sequence 6, Application US/09854845
; GENERAL INFORMATION:
; Patent No. 6750054
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; CURRENT APPLICATION NUMBER: US/09/854, 845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205, 274
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1034
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-6

Query Match 30.0%; Score 6; DB 4; Length 1034;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSSWAL 8
Db 568 WSSWAL 573

RESULT 24
US-09-854-845-4
; Sequence 4, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; CURRENT APPLICATION NUMBER: US/09/854, 845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205, 274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208, 893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1093
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-4

Query Match 30.0%; Score 6; DB 4; Length 1093;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSSWAL 8
Db 612 WSSWAL 617

RESULT 25
US-09-854-845-12
; Sequence 12, Application US/09854845
; Patent No. 6750054

Query Match 30.0%; Score 6; DB 4; Length 1049;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSSWAL 8
Db 568 WSSWAL 573

```

; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 12
; LENGTH: 1136
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-854-845-12

Query Match          30.0%;  Score 6;  DB 4;  Length 1136;
Best Local Similarity 100.0%;  Pred. No. 1.2e+02;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      3 WSSWAL 8
Db     670 WSSWAL 675

RESULT 26
US-09-854-845-10
; Sequence 10. Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 10
; LENGTH: 1151
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-854-845-10

Query Match          30.0%;  Score 6;  DB 4;  Length 1151;
Best Local Similarity 100.0%;  Pred. No. 1.2e+02;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      3 WSSWAL 8
Db     670 WSSWAL 675

RESULT 27
US-09-676-519-27
; Sequence 27. Application US/09676519
; Patent No. 6737508
; GENERAL INFORMATION:
; APPLICANT: PELLETIER, JERRY
; APPLICANT: GROS, PHILLIPPE
; APPLICANT: DUBOW, MICHAEL
; TITLE OF INVENTION: DNA SEQUENCES FROM STAPHYLOCOCCUS AUREUS BACTERIOPHAGES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst

```

```

; TITLE OF INVENTION: 3A, 77, AND 96 THAT ENCODE ANTI-MICROBIAL POLYPEPTIDES
; FILE REFERENCE: 073406-0104
; CURRENT APPLICATION NUMBER: US/09/676,519
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/407,804
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 60/110,992
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 27
; LENGTH: 1509
; TYPE: PRT
; ORGANISM: Staphylococcus bacteriophage
; US-09-676-519-27

Query Match          30.0%;  Score 6;  DB 4;  Length 1509;
Best Local Similarity 100.0%;  Pred. No. 1.5e+02;
Matches 6;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      14 RRYGWG 19
Db     1357 RRYGWG 1362

RESULT 28
US-08-98B-024C-7
; Sequence 7. Application US/089888024C
; Patent No. 6635452
; GENERAL INFORMATION:
; APPLICANT: Monforte, Joseph A.
; APPLICANT: Becker, Christopher H.
; APPLICANT: Pollast, Daniel J.
; APPLICANT: Shaler, Thomas A.
; TITLE OF INVENTION: Releasable No. 6635452volatile Mass-Label Molecules
; FILE REFERENCE: 24736-2057
; CURRENT APPLICATION NUMBER: US/08/98B-024C
; CURRENT FILING DATE: 1997-12-10
; PRIOR APPLICATION NUMBER: US 60/033,037
; PRIOR FILING DATE: 1996-12-10
; PRIOR APPLICATION NUMBER: US 60/046,719
; PRIOR FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
; US-08-98B-024C-7

Query Match          25.0%;  Score 5;  DB 4;  Length 12;
Best Local Similarity 100.0%;  Pred. No. 35;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      12 WLRRY 16
Db     5 WLRRY 9

RESULT 29
US-07-944-143C-21
; Sequence 21. Application US/07944143C
; Patent No. 5719064
; GENERAL INFORMATION:
; APPLICANT: Scofield, R. Hal
; APPLICANT: Harley, John B.
; TITLE OF INVENTION: Peptide Diagnostics and Therapeutics for
; SPONDYLOARTHROPATHIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst

```

STREET: 2800 One Atlantic Center
 STREET: 1201 West Peachtree Street
 CITY: Atlanta
 STATE: GA
 COUNTRY: USA
 ZIP: 30309-3450
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/944,143C
 FILING DATE:
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Pabst, Patrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: OMRF138
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 873-8794
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-07-944-143C-21

Query Match 25.0%; Score 5; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 WLRYY 16
 Db 2 WLRYY 6

RESULT 30
 PCT-US93-08214-21
 Sequence 21, Application PC/TUS9308214
 GENERAL INFORMATION:
 APPLICANT: Oklahoma Medical Research Foundation
 TITLE OF INVENTION: Peptide Diagnostics and Therapeutics
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Kilpatrick & Cody
 STREET: 1100 Peachtree Street, Suite 2800
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: United States
 ZIP: 30309-4530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08214
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Pabst, Patrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: OMRF138
 TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 815-6508
 ; TELEFAX: (404) 815-6555
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; PCT-US93-08214-21

Query Match 25.0%; Score 5; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 WLRYY 16
 Db 2 WLRYY 6

RESULT 31
 US-09-155-613A-6
 Sequence 6, Application US/09155613A
 ; GENERAL INFORMATION:
 ; APPLICANT: Boulonger, Pierre
 ; APPLICANT: Hong, Saw See
 ; APPLICANT: Karayan, Lucie
 ; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
 ; FILE REFERENCE: 02751-036
 ; CURRENT APPLICATION NUMBER: US/09/155-613A
 ; CURRENT FILING DATE: 1998-09-30
 ; PRIOR APPLICATION NUMBER: PCT/FR98/00184
 ; PRIOR FILING DATE: 1998-01-10
 ; PRIOR APPLICATION NUMBER: FR 97/01005
 ; PRIOR FILING DATE: 1997-01-30
 ; PRIOR APPLICATION NUMBER: FR 97/11166
 ; PRIOR FILING DATE: 1997-09-09
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 6
 ; LENGTH: 20
 ; TYPE: RT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic Peptide MH20
 US-09-155-613A-6

Query Match 25.0%; Score 5; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 WLRYY 16
 Db 10 WLRYY 14

RESULT 32
 US-09-498-134A-3
 Sequence 3, Application US/09498134A
 ; Patent No. 6649396
 ; GENERAL INFORMATION:
 ; APPLICANT: Curiel, David T.
 ; APPLICANT: Douglas, Joanne T.
 ; APPLICANT: Krasnykh, Victor N.
 ; APPLICANT: Dmitriev, Igor
 ; TITLE OF INVENTION: Fiber Receptor-Independent System for the Propagation of Adenoviral Vectors
 ; TITLE OF INVENTION: Propagation of Adenoviral Vectors


```

; CURRENT FILING DATE: 1998-09-30
; PRIORITY APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Phagotope
; OTHER INFORMATION: Phagotope
US-09-155-613A-97

RESULT 36
Query Match Score 5; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 WLARRY 16
Db 11 WLARRY 15

RESULT 36
US-09-155-613A-1
; Sequence 1, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; HONG, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-613A-1

Query Match Score 5; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 WLARRY 16
Db 12 WLARRY 16

RESULT 37
US-09-155-613A-98
; Sequence 98, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; HONG, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Phagotope
; OTHER INFORMATION: Phagotope
US-09-155-613A-98

Query Match Score 5; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 WLARRY 16
Db 12 WLARRY 16

RESULT 38
US-09-155-613A-22
; Sequence 22, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; HONG, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: FR 97/01005
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: FR 97/11166
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-613A-22

Query Match Score 5; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 WLARRY 16
Db 10 WLARRY 14

RESULT 39
US-09-155-613A-23
; Sequence 23, Application US/09155613A
; Patent No. 6420120
; GENERAL INFORMATION:
; APPLICANT: Boulanger, Pierre
; HONG, Saw See
; APPLICANT: Karayan, Lucie
; TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
; FILE REFERENCE: 032751-036
; CURRENT APPLICATION NUMBER: US/09/155,613A
; CURRENT FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: PCT/FR98/00184
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-613A-23

```

PRIOR FILING DATE: 1998-01-30
 PRIOR APPLICATION NUMBER: FR 97/01005
 PRIOR FILING DATE: 1997-01-30
 PRIOR APPLICATION NUMBER: FR 97/11166
 PRIOR FILING DATE: 1997-09-09
 PRIOR APPLICATION NUMBER: FR 97/11166
 NUMBER OF SEQ ID NOS: 98
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 23
 LENGTH: 35
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-155-613A-23

Query Match 25.0%; Score 5; DB 4; Length 35;
 Best Local Similarity 100.0%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 WLRYY 16
 Db 25 WLRRY 29

RESULT 40
 US-08-179-632-7
 ; Sequence 7, Application US/08179632
 ; Patent No. 5607914
 ; GENERAL INFORMATION:
 ; APPLICANT: Rao, A. Gururaj; Zhong, Lingxiu
 ; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pioneer Hi-Bred International, Inc.
 ; STREET: 700 Capital Square, 400 Locust Street
 ; CITY: Des Moines
 ; STATE: Iowa
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS/Windows
 ; SOFTWARE: Microsoft Windows No. 5607914epad
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/179, 632
 ; FILING DATE: 07-JAN-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/079, 512
 ; FILING DATE: 06/18/93
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Roth, Michael J.
 ; REGISTRATION NUMBER: 29,342
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (515) 245-3594
 ; TELEFAX: (515) 245-3634
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 38 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; DESCRIPTION: hordothionin derivative

Query Match 25.0%; Score 5; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RWLRR 15
 Db 8 RWLRR 12

RESULT 41
 US-08-440-174A-7
 ; Sequence 7, Application US/08440174A
 ; Patent No. 5717061
 ; GENERAL INFORMATION:
 ; APPLICANT: Rao, Gururaj A.
 ; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
 ; STREET: 7100 N.W. 62nd Avenue
 ; CITY: Johnston
 ; STATE: Iowa
 ; ZIP: 50131
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.3.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/440,174A
 ; FILING DATE: 12-MAY-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/079, 512
 ; FILING DATE: 18-JUN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bobrowicz, Donna
 ; REGISTRATION NUMBER: 32,196
 ; REFERENCE/DOCKET NUMBER: Q234R2D-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (515) 245-4896
 ; TELEFAX: (515) 334-6883
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 38 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

Query Match 25.0%; Score 5; DB 1; Length 38;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RWLRR 15
 Db 8 RWLRR 12

RESULT 42
 PCT-US05-00062-7
 ; Sequence 7, Application PC/TW59500062
 ; GENERAL INFORMATION:
 ; APPLICANT: Pioneer Hi-Bred International, Inc.
 ; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pioneer Hi-Bred International, Inc.
 ; STREET: 700 Capital Square, 400 Locust Street
 ; CITY: Des Moines
 ; STATE: Iowa
 ; ZIP: 50309
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS/Microsoft Windows

SOFTWARE: Microsoft Windows Notepad
 CURRENT APPLICATION DATA: PCT/US95/00062
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Yates, Michael E.; Sweeney, Patricia A.;
 NAME: Robb, Michael J.; & Simon, Somma G.
 REGISTRATION NUMBER:
 REFERENCE DOCKET NUMBER: 234R2-PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (515) 248-4800
 TELEFAX: (515) 248-4844
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: horどothionin derivative
 PCT/US95-00062-7

Query Match 25.0%; Score 5; DB 5; Length 38;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 RMR 15
 Db 8 RMR 12

RESULT 43
 US-09-621-976-4432
 Sequence 4432, Application US/09621976
 Patent No. 6629063
 GENERAL INFORMATION:
 APPLICANT: Dumas Milne Edwards, J.B.
 APPLICANT: Jobert, S.
 APPLICANT: Giordano, J.Y.
 TITLE OF INVENTION: EST's and Encoded Human Proteins.
 FILE REFERENCE: GENSET 054 PR2
 CURRENT APPLICATION NUMBER: US/09/621.976
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 19335
 SEQ ID NO 4432
 LENGTH: 51

TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: 23
 OTHER INFORMATION: Xaa = Ala, Glu, Gly, Val
 NAME/KEY: UNSURE
 LOCATION: 19
 OTHER INFORMATION: Xaa = Ala, Pro, Ser, Thr
 NAME/KEY: UNSURE
 LOCATION: 31
 OTHER INFORMATION: Xaa = Ile, Asn, Ser, Thr
 US-09-621-976-4432

Query Match 25.0%; Score 5; DB 4; Length 51;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SWALG 9
 Db 45 SWALG 49

RESULT 44
 PCT-US94-14074-1
 Sequence 1, Application PC/US9414074
 GENERAL INFORMATION:
 APPLICANT: MakSYMowYCH, Andrew B
 APPLICANT: Hsu, Tin-Chen
 APPLICANT: Jameson, Bradford A
 APPLICANT: Litwack, Gerald A
 TITLE OF INVENTION: Biologically Active Compounds
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
 STREET: One Liberty Place 46th Floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: United States of America
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14074
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/164,102
 FILING DATE: 07-DEC-1993
 CLASSIFICATION:
 NAME: DeLuca, Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TUU-1418
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEFAX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 60 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 PCT-US94-14074-1

Query Match 25.0%; Score 5; DB 5; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ALGWR 11
 Db 55 ALGWR 59

RESULT 45
 US-09-134-001C-3836
 Sequence 3836, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-C-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 3836
 LENGTH: 61

;

;

TYPE: PRT
ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-3836

Query Match Score 5; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 11 RWLRR 15
Db 38 RWLRR 42

RESULT 46
US-09-513-999C-4436
Sequence 4436, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59-US2-REG
CURRENT APPLICATION NUMBER: US 09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: US 60/122,487
PRIORITY FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent-ppm
SEQ ID NO: 4436
LENGTH: 62
TYPE: PRT
ORGANISM: *Homo sapiens*

FEATURE:
NAME/KEY: SIGNAL
LOCATION: -25.-1
OTHER INFORMATION: score 4
OTHER INFORMATION: seq LLQBTGLCMCLLS/PE

US-09-513-999C-4436

Query Match Score 5; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 10 WRWLR 14
Db 33 WRWLR 37

RESULT 47
US-09-252-991A-29873
Sequence 29873, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 29973
LENGTH: 73
TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-29973

Query Match Score 5; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 4 SSWAL 8
Db 36 SSWAL 40

RESULT 50
US-09-270-767-59078
Sequence 59078, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:

Query Match

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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 59078
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-59078

Query Match          25.0%; Score 5; DB 4; Length 79;
Best Local Similarity 100.0%; Prd. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    13 LRRYG 17
      |||||
Db     38 LRRYG 42

RESULT 51
US-09-205-258-403
; Sequence 403, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-16
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (15)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-403

Query Match          25.0%; Score 5; DB 4; Length 82;
Best Local Similarity 100.0%; Prd. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    7 ALGWR 11
      |||||
Db     50 ALGWR 54

RESULT 52
US-09-621-976-3972
; Sequence 3972, Application US/09621976
; Parent No. 6539063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335

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; SOFTWARE: Patent.pm
; SEQ ID NO: 3972
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -36..-1
; NAME/KEY: UNSURE
; LOCATION: 7
; OTHER INFORMATION: Xaa = Arg,Thr
; NAME/KEY: UNSURE
; LOCATION: 24
; OTHER INFORMATION: Xaa = Asn,Thr
; NAME/KEY: UNSURE
; LOCATION: 30
; OTHER INFORMATION: Xaa = Ser,Thr
US-09-621-976-3972

Query Match 25.0%; Score 5; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 SSWAL 8
Db 45 SSWAL 49

RESULT 53
US-09-673-809-25
; Sequence 25, Application US/09673809
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.
; FILE REFERENCE: PCT99 86.HLA
; CURRENT APPLICATION NUMBER: US/09/673..809
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 107
; PRIOR APPLICATION NUMBER: 98870088.6
; PRIORITY: 1998-04-20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 25
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-809-25

Query Match 25.0%; Score 5; DB 4; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 WLRYY 16
Db 77 WLRYY B1

RESULT 54
US-09-652-345-4
; Sequence 4, Application US/09652345
; GENERAL INFORMATION:
; APPLICANT: Farb, David H
; APPLICANT: Russek, Shelley
; APPLICANT: Jang, Ming-Kuei
; APPLICANT: Gibbs, Terrell
; TITLE OF INVENTION: EFFECT OF STEROIDS ON NMDA RECEPTORS DEPENDS ON SUBUNIT
; FILE REFERENCE: 0146-2026
; CURRENT APPLICATION NUMBER: US/09/652..345
; PRIORITY: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/151,802
; PRIOR FILING DATE: 1999-08-31

Query Match 25.0%; Score 5; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      15 RYWGNG 19          ; CURRENT APPLICATION NUMBER: US/09/621,976
Db      97 RYWGNG 101         ; CURRENT FILING DATE: 2000-07-21
                                         ; NUMBER OF SEQ ID NOS: 19335
                                         ; SOFTWARE: Patent.pmm
                                         ; SEQ ID NO: 5890
                                         ; LENGTH: 119
                                         ; TYPE: PRT
                                         ; ORGANISM: Homo sapiens
                                         ; FEATURE:
                                         ; NAME/KEY: SIGNAL
                                         ; LOCATION: -48..-1
                                         ; US-09-621-976-5890

RESULT 57
GENERAL INFORMATION:
; Sequence 7483, Application US/09621976
; Patent No. 6339063
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pmm
; SEQ ID NO: 7483
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-7483

Query Match          25.0%; Score 5; DB 4; Length 113;
Best Local Similarity          100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 QWSS 5             ; QUERY SEQUENCE: QWSS
Db      5 QWSS 9             ; DATABASE SEQUENCE: QWSS
                                         ; Best Local Similarity 100.0%; Score 5; DB 4; Length 119;
                                         ; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                         ; OTHER INFORMATION: Xaa= * or Glu or Lys or Gln
                                         ; US-09-513-959C-5792

RESULT 58
US-09-621-976-5186
GENERAL INFORMATION:
; Sequence 5186, Application US/09621976
; Patent No. 6339063
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pmm
; SEQ ID NO: 5186
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-5186

Query Match          25.0%; Score 5; DB 4; Length 119;
Best Local Similarity          100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      13 LRRYG 17           ; QUERY SEQUENCE: LRRYG
Db      17 LRRYG 21            ; DATABASE SEQUENCE: LRRYG
                                         ; Best Local Similarity 100.0%; Score 5; DB 4; Length 119;
                                         ; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                         ; OTHER INFORMATION: Xaa= * or Glu or Lys or Gln
                                         ; US-09-513-959C-5792

RESULT 59
US-09-621-976-5890
GENERAL INFORMATION:
; Sequence 5890, Application US/09621976
; Patent No. 6339063
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/816,248
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 2

RESULT 60
US-09-513-959C-5792
GENERAL INFORMATION:
; Sequence 5792, Application US/09513999C
; Patent No. 6783961
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ducleir, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/1122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SEQ ID NO: 5792
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 106
; OTHER INFORMATION: Xaa= * or Glu or Lys or Gln
; US-09-513-959C-5792

Query Match          25.0%; Score 5; DB 4; Length 119;
Best Local Similarity          100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      2 VWSW 6              ; QUERY SEQUENCE: VWSW
Db      90 VWSW 94             ; DATABASE SEQUENCE: VWSW
                                         ; Best Local Similarity 100.0%; Score 5; DB 4; Length 119;
                                         ; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                         ; OTHER INFORMATION: Xaa= * or Glu or Lys or Gln
                                         ; US-09-816-248-2

RESULT 61
US-09-816-248-2
GENERAL INFORMATION:
; Sequence 2, Application US/09816248
; Patent No. 6753411
; APPLICANT: BAUMANN, PETER
; APPLICANT: CEBCH, THOMAS R.
; TITLE OF INVENTION: PROTECTION-OF-TELOMERE-1 (POT-1) PROTEIN AND ENCODING
; TITLE OF INVENTION: POLYNUCLEOTIDES
; FILE REFERENCE: 09491/0201
; CURRENT APPLICATION NUMBER: US/09/816,248
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 2

```

LENGTH: 123
 TYPE: PRT
 ORGANISM: *Strychnochia mytilis*
 US-09-816-248-2

Query Match 25.0%; Score 5; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSWAL 8
 Db 117 SSWAL 121

RESULT 62 US-09-816-248-3

Sequence 3, Application US/09816248
 Patent No. 6753411
 GENERAL INFORMATION:
 APPLICANT: BAUMANN, PETER
 APPLICANT: CECH, THOMAS R.
 TITLE OF INVENTION: PROTECTION-OF-TELOMERE-1 (POT-1) PROTEIN AND ENCODING
 FILE REFERENCE: 089491/0201
 CURRENT APPLICATION NUMBER: US/09/816,248
 CURRENT FILING DATE: 2001-03-26
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3
 LENGTH: 123
 TYPE: PRT
 ORGANISM: *Oxytricha trifallax*
 US-09-16-248-3

Query Match 25.0%; Score 5; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSWAL 8
 Db 117 SSWAL 121

RESULT 63 US-09-16-248-4

Sequence 4, Application US/09816248
 Patent No. 6753411
 GENERAL INFORMATION:
 APPLICANT: BAUMANN, PETER
 APPLICANT: CECH, THOMAS R.
 TITLE OF INVENTION: PROTECTION-OF-TELOMERE-1 (POT-1) PROTEIN AND ENCODING
 FILE REFERENCE: 089491/0201
 CURRENT APPLICATION NUMBER: US/09/816,248
 CURRENT FILING DATE: 2001-03-26
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 123
 TYPE: PRT
 ORGANISM: *Oxytricha nova*
 US-09-816-248-4

Query Match 25.0%; Score 5; DB 4; Length 123;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SSWAL 8
 Db 117 SSWAL 121

RESULT 64 US-09-816-248-5

Sequence 5, Application US/09816248
 Patent No. 6753411
 GENERAL INFORMATION:
 APPLICANT: KOHARA, Haruhiko
 APPLICANT: Spivak-Kroizman, Taly
 APPLICANT: Lax, Irit
 APPLICANT: Schlessinger, Joseph
 TITLE OF INVENTION: ADAPTOR PROTEIN FRG2 AND RELATED PRODUCTS AND METHODS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/980,523
 FILING DATE: December 1, 1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/21851
 FILING DATE: December 1, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 230/045
 TELECOMMUNICATION INFORMATION:
 PHONE: (213) 489-1600
 FAX: (213) 955-0440
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 129 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-523-11

Query Match 25.0%; Score 5; DB 3; Length 129;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 LRRYIG 17
 Db 52 LRRYIG 56

RESULT 65 US-09-540-236-3251

Sequence 3251, Application US/09540236
 Patent No. 6753910
 GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709-2005-001
 CURRENT APPLICATION: US/09/540,236
 CURRENT FILING DATE: 2000-04-04
 NUMBER OF SEQ ID NOS: 3840
 SEQ ID NO 3251

RESULT 66

LENGTH: 131
 TYPE: PRT
 ORGANISM: M.catarrhalis
 US-09-540-236-3251

Query Match Score 5; DB 4; Length 131;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSWAL 8
 Db 59 SSWAL 63

RESULT 66

US-09-036-574-4 Application US/09036574

PATENT NO. 6215045

GENERAL INFORMATION:

APPLICANT: (countries other than US) THE UNIVERSITY OF MELBOURNE

APPLICANT: (US only) KNOX, RB; SINGH, MB; and XU, H.

TITLE OF INVENTION: DEVELOPMENTAL REGULATION IN ANTER TISSUE OF PLANTS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY SCOTT MURPHY & PRESSER

STREET: 400 GARDEN CITY PLAZA

CITY: GARDEN CITY

STATE: NEW YORK

COUNTRY: UNITED STATES OF AMERICA

ZIP: 11530-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,294A

FILING DATE: 16-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PL6400

FILING DATE: 15-DEC-1993

APPLICATION NUMBER: AU PL6400

FILING DATE: 16-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: DIGIGLIO, FRANK S.

REFERENCE/DOCKET NUMBER: 9738

TELECOMMUNICATION INFORMATION:

TELEPHONE: + 1 516 742 4343

TELEFAX: + 1 516 742 4366

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-454-294A-4

Query Match Score 5; DB 4; Length 137;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSWAL 8
 Db 119 SSWAL 123

RESULT 68

US-09-270-767-32020

SEQUENCE 32020, Application US/09270767

PATENT NO. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

CURRENT APPLICATION NUMBER: US/09/270-767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO. 32020

LENGTH: 144

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-32020

Query Match Score 5; DB 4; Length 144;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SSWAL 8
 Db 119 SSWAL 123

RESULT 67

US-08-454-294A-4 Application US/08454294A

SEQUENCE 4, Application US/08454294A

```

Db      62  RWLRR 66
RESULT 69
; sequence 47237, Application US/09270767
; Patent No. 6703491
; CURRENT APPLICATION NUMBER: US/09/270/767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 47237
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47237

Query Match          25.0%;  Score 5;  DB 4;  Length 144;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Organism: Pseudomonas aeruginosa
US-09-270-767-47237

RESULT 70
; Sequence 27239, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252-991A-30988
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 27239
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-270-767-47237

Query Match          25.0%;  Score 5;  DB 4;  Length 144;
Best Local Similarity 100.0%;  Pred. No. 2.6e+02;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Organism: Pseudomonas aeruginosa
US-09-270-767-47237

RESULT 71
; Sequence 20364, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252-991A-30988
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 32019
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-270-767-47237

Query Match          25.0%;  Score 5;  DB 4;  Length 168;
Best Local Similarity 100.0%;  Pred. No. 2.9e+02;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Organism: Pseudomonas aeruginosa
US-09-270-767-47237

RESULT 72
; Sequence 30988, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252-991A-30988
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 30988
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-270-767-47237

Query Match          25.0%;  Score 5;  DB 4;  Length 168;
Best Local Similarity 100.0%;  Pred. No. 2.9e+02;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Organism: Pseudomonas aeruginosa
US-09-270-767-47237

RESULT 73
; Sequence 32019, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252-991A-32019
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 32019
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-270-767-47237

Query Match          25.0%;  Score 5;  DB 4;  Length 158;
Best Local Similarity 100.0%;  Pred. No. 2.8e+02;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Organism: Pseudomonas aeruginosa
US-09-270-767-47237

```

Query Match 25.0%; Score 5; DB 4; Length 169;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 14 RRYGW 18
 Db 88 RRYGW 92

RESULT 74
 US-09-252-991A-18579
 ; Sequence 18579, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196..136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; CURRENT FILING DATE: 1998-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18579
 ; LENGTH: 170
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18579

Query Match 25.0%; Score 5; DB 4; Length 170;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 RWLRR 15
 Db 105 RWLRR 109

RESULT 75
 US-09-252-991A-20339
 ; Sequence 20339, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196..136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 20339
 ; LENGTH: 173
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-20339

Query Match 25.0%; Score 5; DB 4; Length 173;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 RWLRR 15
 Db 24 RWLRR 28

Search completed: October 26, 2004, 07:25:04
 Job time : 22.25 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 07:05:46 ; Search time 16.5 Seconds
 (without alignments)
 116.626 Million cell updates/sec

Title: US-10-066-965A-3

Perfect score: 20
 Sequence: 1 PRGAPKWMRWTQMLLETMFL 20

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_79:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	191	2 A552228	fms protein homolo
2	6	30.0	232	2 H72274	polypeptide deform
3	6	30.0	352	2 S17313	transcription fact
4	6	30.0	377	2 A34672	M polypeptide prec
5	6	30.0	1437	2 S07430	L protein - rabies
6	25.0	34	2 PQ0441	L protein - rabies	
7	5	25.0	34	2 P00363	hypothetical prote
8	5	25.0	75	2 T26778	spasmolytic protein
9	5	25.0	77	2 F6919	conserved hypothet
10	5	25.0	99	2 BB2324	hypothetical prote
11	5	25.0	110	2 T17913	hypothetical prote
12	5	25.0	119	2 T08271	probable thiodox
13	5	25.0	123	2 D72579	hypothetical prote
14	5	25.0	128	1 S12372	spasmolytic protein
15	5	25.0	129	1 T53637	hypothetical prote
16	5	25.0	140	2 T33159	hypothetical prote
17	5	25.0	142	2 G82796	hypothetical prote
18	5	25.0	148	2 AH1645	probable thioredox
19	5	25.0	148	2 AD1194	hypothetical prote
20	5	25.0	162	2 D75295	DNA topology modul
21	5	25.0	164	2 A97402	probable N-acetyl
22	5	25.0	164	2 A12619	acetyltransferase
23	5	25.0	169	2 AB2373	polypeptide deform
24	5	25.0	170	2 AF2621	polypeptide deform
25	5	25.0	170	2 F97403	polypeptide deform
26	5	25.0	173	2 G87282	methionyl-tRNA def
27	5	25.0	175	2 B71732	hypothetical prote
28	5	179	2 S58124	auxin-induced prot	
29	5	189	2 S39075		

30	SAVLDL	195	1	SAVLDL
31	delta large antige	195	1	delta large antige
32	auxin-induced prot	195	2	T10941
33	complement compone	195	2	I46888
34	hypothetical prote	202	2	C83079
35	conserved hypothet	209	2	E81014
36	probable pseudourid	220	2	A81959
37	hypothetical prote	220	2	S33204
38	hypothetical prote	230	2	S33734
39	hemagglutinin asso	230	2	S18997
40	nixP2 protein (AJ2	230	2	C98274
41	flagellar protein	254	2	H83954
42	lacto-N-neotetraos	254	2	B81971
43	glycosyl transfera	254	2	C81027
44	glycosyl transfera	254	2	S70814
45	endo-nuclease iv (e	254	2	S70815
46	hypothetical prote	254	2	E90589
47	hypothetical prote	254	2	T27610
48	hypothetical prote	254	2	A81971
49	hypothetical prote	280	2	A81027
50	hypothetical prote	280	2	E70745
51	hypothetical prote	284	2	T22501
52	hypothetical prote	284	2	AB1529
53	hypothetical prote	294	2	C72378
54	hypothetical prote	296	2	T24827
55	hypothetical prote	304	2	G72776
56	hypothetical prote	305	2	T20906
57	hypothetical prote	308	2	A89896
58	hypothetical prote	308	2	H75049
59	hypothetical prote	308	2	G71110
60	hypothetical prote	320	2	A24815
61	hypothetical prote	326	2	H82455
62	hypothetical prote	330	2	T02347
63	hypothetical prote	330	2	AB2574
64	hypothetical prote	344	1	A40005
65	hypothetical prote	351	2	D96761
66	hypothetical prote	355	2	T29932
67	hypothetical prote	357	2	T24137
68	hypothetical prote	364	2	T08903
69	hypothetical prote	368	2	T40115
70	hypothetical prote	382	2	D82264
71	hypothetical prote	394	1	BWHXD
72	hypothetical prote	406	2	S39965
73	hypothetical prote	407	2	T00693
74	hypothetical prote	409	2	T24138
75	hypothetical prote	420	2	D87492
76	hypothetical prote	433	2	T41038
77	hypothetical prote	433	2	T50395
78	hypothetical prote	435	2	GB4518
79	hypothetical prote	443	2	AB2841
80	hypothetical prote	443	2	D97618
81	hypothetical prote	445	2	CB3674
82	hypothetical prote	446	2	T34782
83	hypothetical prote	447	2	E95941
84	hypothetical prote	454	2	AB2364
85	hypothetical prote	455	2	JC1224
86	hypothetical prote	458	2	T31631
87	hypothetical prote	459	2	T16572
88	hypothetical prote	459	2	H81986
89	hypothetical prote	469	2	C81042
90	hypothetical prote	469	2	C82421
91	hypothetical prote	485	2	D84475
92	hypothetical prote	488	2	A27353
93	hypothetical prote	492	2	T16569
94	hypothetical prote	501	2	G95103
95	hypothetical prote	501	2	E91971
96	hypothetical prote	511	2	JC1682
97	hypothetical prote	516	2	T37066
98	hypothetical prote	527	2	E75503
99	hypothetical prote	530	2	G95588
100	hypothetical prote	534	2	S21961

ALIGNMENTS

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-352 <OKA>

A;Cross-references: UNIPROT:P20263; GB:SS58426; NID:9235987; PIDN:AAB19896-1; PID:923598

R;Rosner, M.H.; Vigano, M.A.; Ozato, K.; Timmons, P.M.; Poerier, F.; Rigby, P.W.J.; Stau

C;Species: *Thermus aquaticus*

C;Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 15-Mar-2004

C;Accession: A55228

R;Meinnel, T.; Blanquet, S.

J;Bacteriol, 176, 7387-7390, 1994

A;Title: Characterization of the *Thermus thermophilus* locus encoding peptide deformylase

A;Reference number: A55228; PMID:95050326; PMID:7961514

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-191 <NEIL>

A;Cross-references: GB:X79087; NID:9602912; PIDN:CAAA55695.1; PID:9602914

C;Superfamily: peptide deformylase

Query Match

Score 30.0%; Score 6; DB 2; Length 191;

Best Local Similarity 100.0%; Pred. No. 8.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETMF 19

| | | | |

Db 32 MLETMF 37

Query Match

Score 30.0%; Score 6; DB 2; Length 352;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMFL 20

| | | | |

Db 238 LETMFL 243

RESULT 2

H75274

polypeptide deformylase - *Deinococcus radiodurans* (strain R1)

C;Accession: H75274

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

R;White, O.; Eisen, J.A.; Heidelberger, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Smith, H.O.; Venier, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.

A;Reference number: A75250; PMID:20036896; PMID:10567266

A;Accession: H75274

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-232 <WHI>

A;Cross-references: UNIPROT Q9RRQ4; GB:AE002073; GB:96460244; PIDN:AF1197

C;Superfamily: peptide deformylase

A;Gene: DR2434

A;Map position: 1

C;Genetics:

Query Match

Score 30.0%; Score 6; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETMF 19

| | | | |

Db 62 MLETMF 67

Query Match

Score 30.0%; Score 6; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMFL 20

| | | | |

Db 238 LETMFL 243

RESULT 3

S17313

transcription factor Oct-3, short splice form - mouse

N;Alternate names: NF-3, transcription factor Oct-4

C;Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S17313; S10924; A34206

R;Okamoto, H.; Okamoto, K.; Ishino, F.; Ishino-Kaneko, T.; Takeda, S.; Toyoda, Y.; Muram

EMBO J, 10, 2997-3005, 1991

A;Title: The oct3 gene, a gene for an embryonic transcription factor, is controlled by a

A;Reference number: S17313; PMID:92007744; PMID:1915274

A;Accession: S17313

RESULT 5

S07430

M polyprotein precursor - Germiston virus

N;Contains: Glycoprotein G1; glycoprotein G2; nonstructural protein NS-M

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C;Accession: S07430

R;Pardigon, N.; Viallat, P.; Gerbaud, S.; Girard, M.; Bouley, M.

A;Accession: B82524
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-99 <SMA-
A;Cross-references: UNIPROT:Q9PQ09 ; GB:AE004077 ; PID:99107952 ; PID:AAF8550
A;Experimental source: strain 9a5C
B;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
B;Nunes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrer, R
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferrira, A.J.S.
Submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Frohm, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, F.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, B.E.; Laign
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marinho, C.L.; Marques, M.V.; Martins,
A;Authors: Martins, E.M.F.; Matcukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuchiko, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2711
Query Match 25.0%; Score 5; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 0;
Qy 14 MLETM 18
Db 1 MLETM 5

RESULT 11
T17913 hypothetical protein A410L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17913
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: 218806
A;Accession: T17913
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-110 <GRA>
A;Cross-references: UNIPROT:Q94462 ; EMBL:U42500 ; PID:9428896 ; PID:AA96778.1
C;Genetics:
A;Note: A410_L

Query Match 25.0%; Score 5; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0;
Qy 16 ETMFL 20
Db 67 ETMFL 71

RESULT 12
TC8271 probable thioredoxin - Halobacterium sp. (strain NRC-1) plasmid PNR100
C;Alternates names: hypothetical protein H0606; hypothetical protein H1757
C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08271 ; T08372
R;Ng, W.V.; Ciuffo, S.A.; Smith, T.M.; Bungarner, R.B.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A;Title: Snapshot of a large dynamic replicon in a halophilic archaeon: megaplasmid or m
A;Reference number: 216408 ; PMID:9963795 ; PMID:9847077
A;Accession: T08271
A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-119 <NGM>
A;Cross-references: UNIPROT:O46709 ; EMBL:AF016485 ; PID:92822332 ; HALOSP-H0
A;Experimental source: strain NRC-1
A;Generics: COP1
A;Accession: T08372
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-119 <DAS>
A;Cross-references: EMBL:AF016485 ; PID:92822778 ; PID:92822433 ; HALOSP-H1757
A;Experimental source: strain NRC-1
A;Generics: COP2
C;Genetics: <COP1>
A;Gene: trxA ; HALOSP-H0606
A;Genome: plasmid PNR100
C;Genetics: <COP2>
A;Gene: trxA ; HALOSP-H1757
A;Genome: plasmid PNR100
C;Function:
C;Superfamily: thioredoxin; thioredoxin homology
A;Description: involved in reduction of ribonucleotides, methionine sulfoxide sulfate, a
C;Genetics:
A;Gene: XF2711
Query Match 25.0%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0;
Qy 12 CONLE 16
Db 48 CQMLE 52

RESULT 13
D72579 hypothetical protein APE1016 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72579
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yanazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450 ; MUID:99310339 ; PMID:10382966
A;Accession: D72579
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-123 <KRW>
A;Cross-references: UNIPROT:Q9YAM7 ; DDBJ:AP000062 ; PID:95105244 ; PMID:BAA80921.1 ; PID:d1
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1016

Query Match 25.0%; Score 5; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 5; Conservative 0; Mismatches 0;
Qy 1 PRGAP 5
Db 34 PRGAP 38

RESULT 14
S12372 spasmolytic protein precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 24-May-1996 #text_change 18-Jun-1999
C;Accession: S12372 ; S63937
R;Tomasetto, C.; Rio, M.C.; Gautier, C.; Wolf, C.; Harjuvi, M.; Chambon, P.; Lathe, R.
EMBO J. 9, 407-414, 1990
A;Title: hsp, the domain-duplicated homolog of ps2 protein, is co-expressed with ps2 in
A;Reference number: S12371 ; PMID:90151615 ; PMID:2303034
A;Accession: S12372
A;Molecule type: mRNA
A;Residues: 1-128 <TOM>

A;Cross-references: EMBL:X51697
R;Tomasetto, C.; Rio, M.C.; Gautier, C.; Wolf, C.; Hareveni, M.; Chambon, P.; Lathe, R.
submitted to the EMBL Data Library, December 1993
A;Description: hsp, the domain-duplicated homolog of ps2 protein, is co-expressed with ps2
A;Reference number: S63997
A;Accession: S63997
A;Molecule type: mRNA
A;Residues: 1-10, 'V', 12-128 <TOW>
A;Cross-references: EMBL:X51697; NID:g54165; PIDN:CAA35994.1; PID:g54166
C;Genetics:
A;Genes: msp
C;Function: inhibits gastrointestinal motility and gastric acid secretion
C;Superfamily: spasmolytic protein trefoil homology
C;Keywords: duplication; hormone; pancreas
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-128/Product: spasmolytic protein #status predicted <TRF1>
F;80-120/Domain: trefoil homology <TRF2>
F;28-126,30-57,41-56,51-68,80-106,90-105,100-117/Disulfide bonds: #status predicted
Query Match 25.0%; Score 5; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 2 PRGAP 6
Qy 1 PRGAP 5
Db 2 PRGAP 6

RESULT 15
I53637
spasmolytic polypeptide - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I53637
R;Jeffrey, G.P.; Oates, P.S.; Wang, T.C.; Babynsky, M.W.; Brand, S.J.
Gastroenterology 106, 336-345, 1994
A;Title: Spasmolytic polypeptide: a trefoil peptide secreted by rat gastric mucous cells
A;Reference number: 153637; PMID:94131228; PMID:8299900
A;Accession: I53637
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-129 <RES>
A;Cross-references: UNIPROT:Q09030; GB:M97255; NID:9207049; PIDN:AAA19025.1; PIDN:9207050
C;Superfamily: spasmolytic protein; trefoil homology <TRF1>
F;31-72/Domain: trefoil homology <TRF2>
F;81-121/Domain: trefoil homology <TRF2>

Query Match 25.0%; Score 5; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 3 PRGAP 7

RESULT 16
T33359
hypothetical protein F16G10.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T33359
R;Gattung, S.; Scheet, P.
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33359
R;Gattung, S.; Scheet, P.
C;Description: the sequence of C. elegans cosmid F16G10.
A;Reference number: 221329
A;Accession: T33359
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Residues: 1-140 <GAT>
A;Cross-references: UNIPROT:Q76592; EMBL:AFF077537; PIDN:ACC26275.1; GSPDB:GN00020; CESP:
A;Accession: AH1645

A;Experimental source: strain Bristol N2; clone F16G10
C;Genetics:
A;Map position: 2
A;Introns: 12/1; 31/1; 75/3
Query Match 25.0%; Score 5; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 LETMF 19
Db 25 LETMF 29
Qy 15 LETMF 19
Db 25 LETMF 29

RESULT 17
G82796
hypothetical protein XF0524 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82796
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUD:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
B;Accession: G82796
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-142 <SIM>
A;Cross-references: UNIPROT:Q9PFY2; GB:AE003900; GB:AE003849; NID:99105366; PIDN:AAFB3334
A;Experimental source: strain 9a5c
R;Simson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aciencio, M.; Alvarez, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carrera, D.M.; Carrer, H.
de-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, P.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Matques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Mirack, C.Y.; Miyaki, C.Y.;
Palmieri, D.A.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjorski-Almeida, S.; Vettore, A.L.; Ze
A;Content: annotation
C;Genetics:
A;Gene: XF0524

Query Match 25.0%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 59 PRGAP 63

RESULT 18
AH1645
hypothetical protein lin1705 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Accession: AH1645
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
D.; Domangue-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, I.M.; Karst, U.
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1645

A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-148 <GLA>
A;Cross-references: UNIPROT:Q92B45; GB:AU532022; PIDN:CA96936.1; PMID:91641492; GSPDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1705

Query Match 25.0%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 13 QMLET 17
Db 11 QMLET 15

RESULT 19
AD1594 hypothetical protein lin1293 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1594
R;Glaser, P.; Erangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsihi, H.; Jones, I.M.; Kars, U.
Science 294: 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madlano, E.; Maitournam, A.; Makok, C.; Schlueter, T.; Simoes, N.; Tierriz, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; PMID:21537279; PMID:11679669
A;Accession: AD1594
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <GLA>
A;Cross-references: UNIPROT:Q92C98; GB:AU592022; PIDN:CA96524.1; PMID:916413766; GSPDB:G
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin1293

Query Match 25.0%; Score 5; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 13 QMLET 17
Db 11 QMLET 15

RESULT 20
D75295 DNA topology modulation protein FlaR-related protein - Deinococcus radiodurans (strain R)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75295
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.M.; Shen, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Accession: A75250; PMID:20036896; PMID:10567266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <WHI>
A;Cross-references: UNIPROT:Q9RS54; GB:AE002059; PIDN:AAFL181
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR2273
A;Map position: 1

Query Match 25.0%; Score 5; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 1e+02;

RESULT 21
AD7402 probable N-acetyltransferase (AF232919) [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97402
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouroollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Iappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; PMID:21608551; PMID:11743194
A;Accession: A97402
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-164 <KUR>
A;Cross-references: UNIPROT:QBUIE4; GB:AB007869; PIDN:AAK86170.1; PMID:915155263; GSPDB:G
C;Genetics:
A;Gene: AGR_C_619
A;Map position: circular chromosome

Query Match 25.0%; Score 5; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 16 ETMFL 20
Db 114 ETMFL 118

RESULT 22
AI2619 acetyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI2619
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kucyavini, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Perry, M.; Gordon-Kamm, A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:21608550; PMID:11743193
A;Accession: AI2619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-164 <KUR>
A;Cross-references: UNIPROT:QBUIE4; GB:AE008688; PIDN:AAL41375.1; PMID:917738691; GSPDB:G
C;Genetics:
A;Gene: Atu0353
A;Map position: circular chromosome

Query Match 25.0%; Score 5; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 16 ETMFL 20
Db 114 ETMFL 118

RESULT 23
A82273 polypeptide deformylase VC0046 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: AB2373
 R;Heidelberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; charddon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. L., R.R.; Mekalanos, J.J.; Ventier, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: AB2373
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-169 <KTR>
 A;Cross-references: UNIPROT:Q9KVU3; GB:AB004096; GB:AE003852; NID:g9654440; PIDN:AAF9322
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC046
 A;Map position: 1
 C;Superfamily: peptide deformylase

Query Match 25.0%; Score 5; DB 2; Length 169;
 Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETM 18
 Db 35 MLETM 39

RESULT 24
 polypeptide deformylase def [imported] - *Agrobacterium tumefaciens* (strain C58, DuPont)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AF2621
 R;Wood, D.W.; Seubral, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Erage, G.; Gillett, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 233-233, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A;Reference number: AB2577; MUID:21608550; PMID:11743193
 A;Accession: AF2621
 A;Experimental source: strain C58 (DuPont)
 C;Genetics:
 A;Molecule type: DNA
 A;Residues: 1-170 <KUR>
 A;Cross-references: UNIPROT:Q8UD1; GB:AE008688; PIDN:AAL41388.1; PID:917738706; GSPDB:Q
 Qy 14 MLETM 18
 Db 35 MLETM 39

RESULT 25
 polypeptide deformylase (AF23822) [imported] - *Agrobacterium tumefaciens* (strain C58, C;Species: *Agrobacterium tumefaciens*
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: F97403
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 232-2328, 2001
 A;Title: Genome sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
 A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: F97403
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-170 <KTR>
 A;Cross-references: UNIPROT:Q8UD1; GB:AE007869; PIDN:AAK86183.1; PID:91515278; GSPDB:GN
 C;Species: *Rickettsia prowazekii*
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: GG9282
 C;B.Nierman, W.C.; Felbilyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.I.; B.I. Laub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolomeitsev, D.I.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: GG9282
 A;Molecule type: DNA
 A;Residues: 1-173 <STO>
 A;Cross-references: UNIPROT:Q9ABF5; GB:AE005673; PIDN:AAK22259.1; PIDN:913421407; NID:g13421407; NID:913421407
 C;Genetics:
 A;Gene: CC0272
 A;Status: preliminary
 A;Superfamily: peptide deformylase

Query Match 25.0%; Score 5; DB 2; Length 173;
 Best Local Similarity 100.0%; Pred. No. 1.e+02; Indels 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETM 18
 Db 35 MLETM 43

RESULT 27
 methionyl-tRNA deformylase (def) RP208 - *Rickettsia prowazekii*
 C;Species: *Rickettsia prowazekii*
 C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
 C;Accession: B71732
 R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U. M.; Nature 396, 133-140, 1998
 A;Title: The Genome sequence of *Rickettsia prowazekii* and the origin of mitochondria.
 A;Reference number: A71732
 A;Accession: B71732
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-175 <AND>
 A;Cross-references: UNIPROT:Q92DV8; GB:AJ235270; GB:AJ235269; PIDN:CAA1467;
 A;Experimental source: strain Madrid B
 C;Genetics:
 A;Gene: def; RP208
 C;Superfamily: peptide deformylase

Query Match 25.0%; Score 5; DB 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 1.e+02; Indels 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETM 18
 Db 35 MLETM 39

Qy 14 MLETM 18 C;Accession: A36409
 Db 35 MLETM 39 R;Imazaki, F.; Omata, M.; Ohto, M.
 J;Virol. 64, 5594-5599, 1990
 A;Title: Heterogeneity and evolution rates of delta virus RNA sequences.
 S58124
 RESULT 28
 hypothetical protein - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
 C;Accession: S58124
 R;Blaszyk, R.; Loehiger, C.; Wehling, J.
 submitted to the EMBL Data Library, July 1995
 A;Reference number: S58124
 A;Accession: S58124
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-179 <BLA>
 A;Cross-references: UNIPROT:Q29839; EMBL:X89707; NID:q1052702; PID:CAA61854.1; PMID:9105
 C;Genetics:
 A;Introns: 89/2

Query Match 25.0%; Score 5; DB 1; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 159 PRGAP 163

RESULT 31
 SAVLDS
 delta large antigen - hepatitis delta virus (isolate Japanese S-1)
 N;Alternative names: HDag
 C;Species: hepatitis delta virus
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: B36409; S18678
 R;Imazaki, F.; Omata, M.; Ohto, M.
 J;Virol. 64, 5594-5599, 1990
 A;Title: Heterogeneity and evolution rates of delta virus RNA sequences.
 A;Reference number: A36409
 A;Accession: B36409
 A;Molecule type: genomic RNA
 A;Residues: 1-195 <IMAI>
 C;Cross-references: UNIPROT:P25883; GB:D90192; GB:M58303; NID:q221695; PMID:BAA14216.1;
 A;Experimental source: isolate Japanese S-1
 R;Imazaki, F.; Omata, M.; Ohto, M.
 Nucleic Acids Res. 19, 5439, 1991
 A;Title: Complete nucleotide sequence of hepatitis delta virus RNA in Japan.
 A;Reference number: S18678
 A;Accession: S18678
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: genomic RNA
 A;Residues: 1-195 <IMAI>
 A;Cross-references: EMBL:X60193; NID:g59497; PID:CAA42749.1; PMID:g59498
 A;Experimental source: isolate Japanese S-1
 A;Note: note this sequence was submitted to the EMBL Data Library, June 1991
 C;Species: hepatitis delta virus large antigen
 C;Keywords: core protein
 F;2-195/Product: delta large antigen #status predicted <IMAI>

Query Match 25.0%; Score 5; DB 1; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 159 PRGAP 163

RESULT 32
 T10941
 auxin-induced protein Aux22 - mung bean
 C;Species: Vigna radiata (mung bean)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C;Accession: T10941
 R;Yamamoto, K.
 submitted to the EMBL Data Library, February 1993
 A;Reference number: Z17205
 A;Accession: T10941
 A;Status: preliminary; translated from GB/EMBL/DDBJ

Qy 15 LETMF 19
 Db 123 LETMF 127

RESULT 30
 SAVLDM
 delta large antigen - hepatitis delta virus (strain Japanese M-1)
 N;Alternative names: HDag
 C;Species: hepatitis delta virus
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

A;Molecule type: mRNA
A;Residues: 1-196 <YAM>
A;Cross-references: UNIPROT:P22294; EMBL:D14413
A;Experimental source: hypocotyl
C;Genetics:
A;Gene: arg4
C;Superfamily: auxin-induced protein aux28

Query Match 25.0%; Score 5; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19
Db 130 LETMF 134

RESULT 35
E81014 conserved hypothetical protein NMB2018 [imported] - *Neisseria meningitidis* (strain MC58)
C;Species: *Neisseria meningitidis*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: E81014
C;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vaithyanathan, J.; Gill, J.; Scariato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: E81014
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-220 <TET>
A;Cross-references: UNIPROT:Q9JXJ0; GB:AE002552; PIDN:AAF42343
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB2018

Query Match 25.0%; Score 5; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETMFL 20
Db 173 ETMFL 177

RESULT 36
A81959 probable pseudouridine synthase NMA0422 [imported] - *Neisseria meningitidis* (strain Z2491
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A81959
C;Parbhill, J.; Achtermann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jageis, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, N.; Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81959
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-220 <PAR>
A;Cross-references: UNIPROT:Q9JWE2; GB:AL162753; PIDN:CAB83721
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA0422

Query Match 25.0%; Score 5; DB 2; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETMFL 20
Db 173 ETMFL 177

RESULT 37
S33204 hypothetical protein - long-stalked stitichwort
C;Species: *Stellaria longipes* (long-stalked stitichwort)
C;Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S33204
R;Zhang, X.H.
A;Reference number: S33204
A;Accession: S33204
A;Status: Preliminary
A;Molecule type: mRNA

Query Match 25.0%; Score 5; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 RWVCO 13
Db 31 RWVCO 35

RESULT 38
C83079 hypothetical protein PA4535 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C;Species: *Pseudomonas aeruginosa*
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83079
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lazebny, K.; Lim, J.; Lozy, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83079
A;Status: Preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9HYP2; GB:AE004867; PIDN:AAGG792
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA4535

Query Match 25.0%; Score 5; DB 2; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Residues: 1-222 <ZHA>
A;Cross-references: UNIPROT:Q41348; EMBL:X71601; NID:g297175; PID:g297176
C;Superfamily: hypothetical protein Hil647

Query Match Score 5; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 54 PRGAP 58

RESULT 38
S37734 hypothetical protein - *Vibrio cholerae*
C;Species: *Vibrio cholerae*
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
R;Fratzon, V.L.; Barker, A.; Manning, P.A.
Infect Immun. 61, 3032-3037, 1993
A;Title: Nucleotide sequence encoding the mannose-tucose-resistant hemagglutinin of *Vibrio cholerae*
A;Reference number: S377340; MUID:93293328; PMID:8514410
A;Accession: S37734
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <PFA>
C;Cross-references: UNIPROT:Q56638; EMBL:X64097
C;Superfamily: type II site-specific DNA-methyltransferase

Query Match Score 5; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETMFL 20
Db 101 ETMFL 105

RESULT 40
C98274 nikP2 protein [AJ250581] [Imported] - *Agrobacterium tumefaciens* (strain C5B, Cereon)
C;Species: *Agrobacterium tumefaciens*
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 12-Jul-2004
C;Accession: C98274
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quirollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C98274
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <KUR>
A;Cross-references: UNIPROT:Q8U9P1; GB:AE007870; PID:AAK897171; PID:915159631; GSPDB:G
C;Genetics:

Qy 2 RGAMP 6
Db 3 RGAMP 7

RESULT 41
H83954 flagellar protein required for flagellar formation flIR [Imported] - *Bacillus halodurans*
C;Species: *Bacillus halodurans*
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83954
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirai, Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A;Reference number: A83650; MUID:20512382; PMID:11058132
A;Accession: H83954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <STO>
A;Cross-references: UNIPROT:Q9KA50; GB:AP001515; GB:BA000004; PID:g10174886; PIDN:BAE061
C;Genetics:
A;Gene: fir

Query Match Score 5; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETM 18
Db 244 MLETM 248

RESULT 39
S18997 hemagglutinin associated protein VCA0447 [Imported] - *Vibrio cholerae* (strain N16961 ser
C;Species: *Vibrio cholerae*
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S18997; H82460
R;van Dongen, W.M.A.; van Vlerken, M.M.A.; de Graaf, F.K.
submitted to the EMBL DNA Library, September 1991
A;Description: Nucleotide sequence of a DNA fragment encoding a *Vibrio cholerae* haemaggly
A;Reference number: S18996
A;Accession: S18997
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <VAN>
A;Cross-references: UNIPROT:Q56638; EMBL:X64387; NID:g48355; PID:CAA45727.1; PID:948357
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
charlson, D.; Ermolaeva, M.D.; Vanathavan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
Nature 406, 477-483, 2000
A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <HEI>
A;Cross-references: GB:AB004377; GB:AB003853; NID:g9657831; PIDN:AAF96353.1; GSPDB:GN001
C;Genetics:
A;Gene: VCA0447
A;Map position: 2
C;Superfamily: type II site-specific DNA-methyltransferase

Query Match Score 5; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
A;Accession: B81971
A;Cross-references: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0447
A;Map position: 2
C;Superfamily: type II site-specific DNA-methyltransferase

Query Match Score 5; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A;Reference number: A81775; MUID:10761919
 A;Accession: BB1971

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-268 <PAR>

A;Cross-references: UNIPROT:Q9JW65; GB:AL162753; GB:AL157959; NID:97379120; PIDN:CAB8381

A;Experimental source: serogroup A, strain Z2491
 C;Genetics:

A;Gene: lgtA2'; NMA0527

C;Superfamily: lipopolysaccharide biosynthesis-associated protein
 C;Species: *Neisseria meningitidis*

Query Match 25.0%; Score 5; DB 2; Length 268;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19

Db 121 LETMF 125

RESULT 43

C81027 Lacto-N-neotetraose biosynthesis glycosyl transferase LgtB NMB1928 [Imported] - *Neisseria meningitidis*
 C;Species: *Neisseria meningitidis*

C;Accession: C81027 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Hiri, H.; Qin, H.; Vaithayanathan, J.; Gill, J.; Scariato, V.; Masignani, V.; Piazza, M.

Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; ve A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307

A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-275 <NET>
 A;Cross-references: UNIPROT:Q51116; GB:AE002098; NID:97227175; PIDN:AAF4225

A;Experimental source: serogroup B, strain MC58
 C;Genetics:

A;Gene: NM1928

C;Superfamily: lipopolysaccharide biosynthesis-associated protein
 C;Species: *Neisseria meningitidis*

Query Match 25.0%; Score 5; DB 2; Length 275;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19

Db 121 LETMF 125

RESULT 44

S70814 Glycosyl transferase B (EC 2.4.1.-) - *Neisseria meningitidis*
 C;Species: *Neisseria meningitidis*

C;Accession: S70814 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
 R;Jennings, M.P.; Hood, D.W.; Peak, I.R.A.; Virji, M.; Moxon, E.R.

Mol. Microbiol. 18, 729-740, 1995
 A;Title: Molecular analysis of a locus for the biosynthesis and phase-variable expression
 A;Reference number: S70812; MUID:96414473; PMID:8817494

A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-275 <JEN>
 A;Cross-references: UNIPROT:Q51116; EMBL:U25839; PIDN:9573183; PIDN:AC44086.1; PIDN:AC44086.1; PIDN:9973183; PIDN:G973183

C;Genetics:
 A;Gene: lgtB
 C;Superfamily: lipopolysaccharide biosynthesis-associated protein
 C;Keywords: glycosyltransferase

Query Match 25.0%; Score 5; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19

Db 117 LETMF 121

RESULT 45

S70815 Glycosyl transferase E (EC 2.4.1.-) - *Neisseria meningitidis*
 C;Species: *Neisseria meningitidis*

C;Accession: S70815 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
 R;Jennings, M.P.; Hood, D.W.; Peak, I.R.A.; Virji, M.; Moxon, E.R.

Mol. Microbiol. 18, 729-740, 1995
 A;Title: Molecular analysis of a locus for the biosynthesis and phase-variable expression
 A;Reference number: S70812; MUID:96414473; PMID:8817494

A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-276 <JEN>
 A;Cross-references: UNIPROT:Q51117; EMBL:U25839; PIDN:9573183; PIDN:AC44086.1; PIDN:9973183

C;Genetics:
 A;Gene: lgtE
 C;Superfamily: lipopolysaccharide biosynthesis-associated protein
 C;Keywords: glycosyltransferase

Query Match 25.0%; Score 5; DB 2; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETM 18

Db 143 MLETM 147

RESULT 47

T27610 hypothetical protein ZC477.8 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T27610

R;Dn: Z

Submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid ZC477.

A;Reference number: Z20392

A;Accession: T27610

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-278 <DUZ>

A;Cross-references: EMBL:U40802; PIDN:AAA81511.1; CESP:ZC477.8

A;Gene: CESP:ZC477.8

A;Introns: 77/1

Query Match 25.0%; Score 5; DB 2; Length 278;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5

Db 112 PRGAP 116

RESULT 48

A81971

Lacto-N-neotetraose biosynthesis glycosyl transferase NMA0525 [imported] - *Neisseria meningitidis* serogroup A strain 22491. C;Species: *Neisseria meningitidis* [imported] - *Neisseria meningitidis* serogroup A strain 22491. C;Cross-references: UNIPROT:P57033; GB:AL157959; NID:97379120; PMID:CA88381

A;Accession: A81971

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-219 <PAR>

A;Experimental source: serogroup A, strain 22491

A;Gene: 1qRB; NMA0525

C;Superfamily: lipopolysaccharide biosynthesis-associated protein

Query Match 25.0%; Score 5; DB 2; Length 279;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19

Db 121 LETMF 125

RESULT 49

A81027

Lacto-N-neotetraose biosynthesis glycosyl transferase LgtE NMB1926 [imported] - *Neisseria meningitidis* serogroup A [imported] - *Neisseria meningitidis* serogroup A. C;Accession: A81027 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masignani, V.; Bizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Verri, H.

A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.

A;Accession: A81000; PMID:20175755; PMID:1071307

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-280 <TER>

A;Cross-references: UNIPROT:Q51117; GB:AE002541; GB:AE002098; NID:97227175; PMID:AAF4225

A;Experimental source: serogroup B, strain MC58

C;Genetics: A;Gene: NMB1926 C;Superfamily: lipopolysaccharide biosynthesis-associated protein

C;Accession: E70745

C;Species: *Mycobacterium tuberculosis* (strain H37RV)

C;Accession: E70745

RESULT 52
 AB1529 transcription regulator (repressor) homolog lin0770 [imported] - *Listeria innocua* (strain C; Species: *Listeria innocua*
 C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C; Accession: AB1529 R; Glaser, P.; Frangeul, L.; Buchrieser, C.; Amand, A.-i.; Baquero, F.; Berche, P.; Bloecker i.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsbhi, H. D.; Jones, L.M.; Karsf., U. Science 29, 849-852, 2001
 A; Authors: Kreft, J.; Kunr, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourna, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A; Title: Comparative Genomics of *Listeria* species.
 A; Reference number: AB1077; MUID:211679659
 A; Accession: AB1529 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-288 <GLA>
 A; Cross-references: UNIPROT:Q92DP3; GB:AU592022; PIDN:CA96002.1; PMID:11679659
 A; Experimental source: strain Clip11262 C; Genetics:
 A; Gene: lin0770 C; Superfamily: glucose kinase; Glucose Kinase homology

Query Match 25.0%; Score 5; DB 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 LETMF 19 Db 209 LETMF 213

RESULT 53
 C72378 sugar ABC transporter, permease protein - *Thermotoga maritima* (strain MSB8)
 C; Species: *Thermotoga maritima*
 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C; Accession: C72378 R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M. Nature 399, 323-329, 1999
 A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A; Reference number: A72200; MUID:92287316; PMID:10360571
 A; Accession: C72378 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-224 <ARN>
 A; Cross-references: UNIPROT:Q9WYQ0; GB:AE000512; PIDN:AA000512; PMID:94980922; PIDN:AA03550 C; Genetics:
 A; Gene: TM0419 C; Superfamily: inner membrane protein uGPA

Query Match 25.0%; Score 5; DB 2; Length 294;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 APWWM 8 Db 149 APWWM 153

RESULT 54
 T24827 hypothetical protein T11B7.3 - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C; Accession: T24827 R; Gardner, A. submitted to the EMBL Data Library, September 1995

A; Reference number: 219940
 A; Accession: T24827 A; Status: Preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA A; Residues: 1-236 <WIL>
 A; Cross-references: UNIPROT:Q22389; EMBL:Z54237; PIDN:CA90989.1; GSPDB:GN00022; CESP:T11
 A; Experimental source: clone T11B7 C; Genetics:
 A; Gene: CESP:T11B7.3
 A; Map position: 4 A; Introns: 45/3; 111/1; 270/1

Query Match 25.0%; Score 5; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5 Db 250 PRGAP 254

RESULT 55
 G72776 hypothetical protein APE0201 - *Aeropyrum pernix* (strain K1)
 C; Species: *Aeropyrum pernix*
 C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C; Accession: G72776 R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Hikawa, Y.; Jin-no, K.; Takahashi, awa, H.; Takamiya, M.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Ki DNA Res. 6, 83-101, 1999
 A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyrum*
 A; Reference number: A72450; MUID:9310339; PMID:10382966
 A; Accession: G72776 A; Status: Preliminary A; Molecule type: DNA A; Residues: 1-304 <WIL>
 A; Cross-references: UNIPROT:Q9YYP8; DDBJ:AP000058; PIDN:BA979113.1; PID: d1 (A; Experimental source: strain K1 C; Genetics:
 A; Gene: APE0201

Query Match 25.0%; Score 5; DB 2; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGAPM 6 Db 156 RGAPM 160

RESULT 56
 T20906 hypothetical protein F14F7.1 - *Caenorhabditis elegans*
 C; Species: *Caenorhabditis elegans*
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C; Accession: T20906 R; McMurray, A. Submitted to the EMBL Data Library, November 1996
 A; Status: Preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-105 <WIL>
 A; Cross-references: UNIPROT:O17805; EMBL:Z81503; PIDN:CA0411.1; GSPDB:GN00021; CESP:F14
 C; Genetics:
 A; Gene: CESP:F14F7.1
 A; Map position: 3 A; Introns: 27/3; 49/3

Query Match 25.0%; Score 5; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

M.; Ohnishi, Y.; Funahashi, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998	A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon, Pyrococcus horikoshii	A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: G71110	A;Status: preliminary; nucleic acid sequence not shown; translation not shown	
A;Molecule type: DNA		
A;Residues: 1-308 <KAW>		
A;Cross-references: UNIPROT:Q9YUN8 ; GB:BA0000018; PIDN:913701030; PIDN:BAB42325.1; GSPDB:G71110	A;Experimental source: strain N315	
A;Cross-references: UNIPROT:Q9YUN8 ; GB:BA0000018; PIDN:913701030; PIDN:BAB42325.1; GSPDB:G71110	A;Experimental source: strain N315	
A;Cross-references: UNIPROT:Q9YUN8 ; GB:BA0000018; PIDN:913701030; PIDN:BAB42325.1; GSPDB:G71110	A;Experimental source: strain N315	
RESULT 57		
A89896	C;Species: Staphylococcus aureus	
C;Accession: A89896	C;Accession: A89896	
C;Citation: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004	C;Citation: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004	
Query Match Score 5; DB 2; Length 308;	Query Match Score 5; DB 2; Length 308;	
Best Local Similarity 100.0%; Pred. No. 1.7e+02;	Best Local Similarity 100.0%; Pred. No. 1.7e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 2 RGAPM 6	Qy 2 RGAPM 6	
Db 181 RGAPM 185	Db 181 RGAPM 185	
RESULT 58		
H75049	C;Species: Pyrococcus abyssi	
C;Accession: H75049	C;Accession: H75049	
C;Citation: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004	C;Citation: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004	
Query Match Score 5; DB 2; Length 308;	Query Match Score 5; DB 2; Length 308;	
Best Local Similarity 100.0%; Pred. No. 1.7e+02;	Best Local Similarity 100.0%; Pred. No. 1.7e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 15 LETMF 19	Qy 15 LETMF 19	
Db 45 LETMF 49	Db 45 LETMF 49	
RESULT 59		
G71110	C;Species: Pyrococcus abyssi	
C;Accession: G71110	C;Accession: G71110	
C;Citation: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004	C;Citation: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004	
Query Match Score 5; DB 2; Length 308;	Query Match Score 5; DB 2; Length 308;	
Best Local Similarity 100.0%; Pred. No. 1.7e+02;	Best Local Similarity 100.0%; Pred. No. 1.7e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 2 RGAPM 6	Qy 2 RGAPM 6	
Db 181 RGAPM 185	Db 181 RGAPM 185	
RESULT 60		
A24815	C;Species: Oryctolagus cuniculus (domestic rabbit)	
C;Accession: A24815; A41418	C;Accession: A24815; A41418	
C;Citation: 24-Jan-1988 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004	C;Citation: 24-Jan-1988 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004	
Query Match Score 5; DB 2; Length 308;	Query Match Score 5; DB 2; Length 308;	
Best Local Similarity 100.0%; Pred. No. 1.7e+02;	Best Local Similarity 100.0%; Pred. No. 1.7e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 2 RGAPM 6	Qy 2 RGAPM 6	
Db 181 RGAPM 185	Db 181 RGAPM 185	
RESULT 61		
AB2574	C;Species: Nostoc sp. PCC 7120	
C;Accession: AB2574	C;Accession: AB2574	
C;Citation: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004	C;Citation: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004	
Query Match Score 5; DB 2; Length 320;	Query Match Score 5; DB 2; Length 320;	
Best Local Similarity 100.0%; Pred. No. 1.8e+02;	Best Local Similarity 100.0%; Pred. No. 1.8e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 15 LETMF 19	Qy 15 LETMF 19	
Db 288 LETMF 292	Db 288 LETMF 292	

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:2159825; PMID:11759810
A;Accession: AB2574
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-325 <KUR>
A;Cross-references: UNIPROT:QBYJU6; GB:AP003605; PIDN:BAB77503.1; PID:917134948; GSPPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr2017
A;Genome: plasmid

Query Match 25.0%; Score 5; DB 2; Length 325;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QMLET 17
Db 228 QMLET 232

RESULT 62

H82455 IS5 transposase VCA0472 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1
C;Species: *Vibrio cholerae*
C;Accession: HB2455; DB2478
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Cross-references: UNIPROT:Q9K2I8; GB:AE004379; GB:AE003853; NID:99657865; PIDN:AAF9637
A;Experimental source: both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: AB2035; MUID:20406833; PMID:1092301
A;Accession: HB2455
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <HE1>
A;Cross-references: UNIPROT:Q9K2I8; GB:AE004379; GB:AE003853; NID:99657865; PIDN:AAF96191.1; GSPPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
A;Accession: DB2478
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-326 <HE2>
A;Experimental source: GB:AE004368; GB:AE004368; NID:99657677; PIDN:AAF96191.1; GSPPDB:GN001
C;Genetics: <GEN1>
A;Gene: VCA0472
A;Map Position: 2
C;Genetics: <GEN2>
A;Gene: VCA028
A;Map Position: 2
C;Superfamily: transposase ISS

Query Match 25.0%; Score 5; DB 2; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LETMF 19
Db 57 LETMF 61

RESULT 63

T02347 probable lipid transfer protein T85.2 - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02347
R;Vysotskaiia, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Liu, S.; Li, J.; Araujo, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Eckert, J.R.; Federspiel, N.A.; Theodorou, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: AB6141; MUID:21016719; PMID:11130712

RESULT 64

A4005 Hyoscyamine (6S)-dioxygenase (EC 1.14.11.11) - henbane
C;Species: *Hyoscyamus niger* (henbane)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A40005
R;Matsuda, J.; Okabe, S.; Hashimoto, T.; Yamada, Y.
J. Biol. Chem. 266, 9460-9464, 1991
A;Title: Molecular cloning of hyoscyamine 6beta-hydroxylase, a 2-oxoglutarate-dependent oxygenase from *Hyoscyamus niger*.
A;Reference number: A40005; MUID:91236712; PMID:2033047
A;Accession: A4005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-344 <MAT>
A;Cross-references: UNIPROT:P24397; GB:MG2719; NID:9168267; PIDN:AAA33387.1; PMID:9168268
C;Superfamily: 1-aminoacyclopropane-1-carboxylate oxidase
C;Keywords: ascorbic acid; iron; metalloprotein; oxidoreductase
F;166,217,274/Binding site: iron (His) #status predicted

Query Match 25.0%; Score 5; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MLETM 18
Db 73 MLETM 77

RESULT 65

D36761 unknown protein [imported] - *Arabidopsis thaliana* (mouse-ear cress)
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: D36761
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A;Reference number: AB6141; MUID:21016719; PMID:11130712

RESULT 66

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-351 <STO>
A;Cross-references: UNIPROT:Q9FX40; GB:AB005173; PIDN:AFG30969.1; GSPPDB:GN
C;Genetics:
A;Gene: T9L24.34
A;Map position: 1

A;Reference number: Z14666

Query Match Score 5; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 QMLET 17
 Db 321 QMLET 325

RESULT 66
 T29932 hypothetical protein F29B9.9 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Accession: T29932
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 R;Goela, D.; Gattung, S.
 submitted to the EMBL Data Library, September 1996
 A;Description: The sequence of *C. elegans* cosmid F29B9.
 A;Reference number: Z20710
 A;Accession: T29932
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-355 <GOB>
 A;Cross-references: UNIPROT:Q9GYI3; EMBL:U70849; PIDN:AAB09121.1; GSPDB:GN00022; CESP:F2
 A;Experimental source: strain Bristol N2; clone F29B9
 C;Genetics:

A;Gene: CESP:F29B9.9
 A;Map Position: 4
 A;Introns: 92/1
 Query Match Score 5; DB 2; Length 355;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 175 PRGAP 179

RESULT 67
 T24137 hypothetical protein R10B4.2a - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Accession: T24137
 R;Ainscough, R.
 submitted to the EMBL Data Library, August 1995
 A;Reference number: Z19843
 A;Accession: T24137
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-357 <WIL>
 A;Cross-references: UNIPROT:Q21900; EMBL:Z50874; PIDN:CRA90772.1; GSPDB:GN00021; CESP:R1
 C;Genetics:
 A;Gene: CESP:R10B4.2a
 A;Map position: 3
 A;Introns: 42/3; 80/3; 249/3; 349/3
 C;Superfamily: ribonucleoprotein repeat homology

Query Match Score 5; DB 2; Length 357;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 QMLET 17
 Db 176 QMLET 180

RESULT 70
 D82264 probable exopolysaccharide biosynthesis protein EpsF VC0920 [imported] - *Vibrio cholerae*
 C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82264
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

RESULT 68
 T8903 hypothetical protein T32A16.10 - *Arabidopsis thaliana*

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. A;Title: DNA Sequence of both chromosomes of the cholera pathogen <i>Vibrio cholerae</i> . A;Reference number: A62035; MUID:20406833; PMID:10552301	Db		242	PRGAP 246	
A;Status: preliminary A;Molecule type: DNA A;Residues: 1-382 <HEI> A;Cross-references: UNIPROT:Q9KTI2; GB:AE004175; PIDN:AAFF408 C;Genetics: A;Gene: VC0920 A;Map position: 1	RESULT 73 TO0693 Hypothetical protein At2g44130 [imported] - <i>Arabidopsis thaliana</i> N;Alternative names: hypothetical protein F6E13.26 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004 C;Accession: T00693; G84874 C;Rounsley, S.D.; Kaul, S.; Lin, X.; Crosby, M.L.; Brandon, R.C.; Sykes, E.R.; Rounsley, S.D.; Kaul, S.; Lin, X.; Crosby, M.L.; Brandon, R.C.; Sykes, E.R.; Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence. A;Accession number: Z114180 A;Description: translated from GB/EMBL/DBJ A;Accession: T00693 A;Molecule type: DNA A;Residues: 1-407 <RCU> A;Cross-references: UNIPROT:O80582; EMBL:AC004005; NID:93212846; PID:93212866				
Query Match 25.0%; Score 5; DB 2; Length 382; Best Local Similarity 100.0%; Pred. No. 2e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db		26	VCQML 30	
Qy 11 VCQML 15 Db 26 VCQML 30	RESULTS 71 R;Kroll, J.S./Lyonds, B.; Brophy, L.N.; Moxon, E.R. Mol. Microbiol. 4, 1853-1862, 1990 A;Title: The box locus in encapsulated Haemophilus influenzae: a chromosomal region involved in capsule formation. A;Reference number: S12232; MUID:91186821; PMID:2083145 A;Accession: S12232 A;Molecule type: DNA A;Residues: 1-394 <KHO> A;Cross-references: UNIPROT:P22236; EMBL:X54987; PIDN:CAA38730.1; PID:g45296 C;Genetics: A;Gene: boxD C;Superfamily: boxD protein	R;Kroll, J.S.; Lyonds, B.; Brophy, L.N.; Moxon, E.R.; Mol. Microbiol. 4, 1853-1862, 1990 A;Title: The box locus in encapsulated Haemophilus influenzae: a chromosomal region involved in capsule formation. A;Reference number: S12232; MUID:91186821; PMID:2083145 A;Accession: S12232 A;Molecule type: DNA A;Residues: 1-394 <KHO> A;Cross-references: UNIPROT:P22236; EMBL:X54987; PIDN:CAA38730.1; PID:g45296 C;Genetics: A;Gene: boxD C;Superfamily: boxD protein	Query Match 25.0%; Score 5; DB 2; Length 407; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULTS 71 R;Ainscough, R. C;Species: Caenorhabditis elegans C;Accession: T24138 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004 C;Cross-references: GB/EMBL/DBJ A;Residues: 1-409 <WIL> A;Experimental source: clone R10E4.2b C;Genetics: A;Gene: CESP:R10B4.2b A;Map Position: 3 B;Introns: 42/3; 106/3; 301/3; 401/3 C;Superfamily: ribonucleoprotein repeat homology	
Query Match 25.0%; Score 5; DB 1; Length 394; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db		16 ETMFL 20 Db 344 ETMFL 348	RESULTS 72 S39965 hypothetical protein - <i>Streptomyces griseus</i> C;Species: Streptomyces griseus C;Accession: S39965 R;Kruegel, H.; Schumann, G.; Haenel, P.; Fiedler, G. Mol. Gen. Genet. 241, 193-202, 1993 A;Title: Nucleotide sequence analysis of five putative <i>Streptomyces griseus</i> genes, one involved in TDP-dauenosine formation. A;Reference number: S39963; MUID:94049680; PMID:8232204 A;Accession: S39965 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-406 <KU> A;Cross-references: UNIPROT:Q54197; EMBL:X73148; PIDN:CAA51670.1; PID:g4078 C;Superfamily: acyl-coa dehydrogenase	Query Match 25.0%; Score 5; DB 2; Length 406; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5	Qy 13 QMLET 17 Db 202 QMLET 206	RESULTS 72 S39965 hypothetical protein At2g44130 [imported] - <i>Arabidopsis thaliana</i> N;Alternative names: hypothetical protein F6E13.26 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004 C;Accession: T00693; G84874 C;Rounsley, S.D.; Kaul, S.; Lin, X.; Crosby, M.L.; Brandon, R.C.; Sykes, E.R.; Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence. A;Accession number: Z114180 A;Description: translated from GB/EMBL/DBJ A;Accession: T00693 A;Molecule type: DNA A;Residues: 1-407 <RCU> A;Cross-references: UNIPROT:O80582; EMBL:AC004005; NID:93212846; PID:93212866	Query Match 25.0%; Score 5; DB 2; Length 409; Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

RESULT 75
D87492 hypothetical protein CC1961 [Imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87492
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Debay, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonin, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Accession number: A87249; PMID:21173698; PMID:11259647
A;Accession: D87492
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-420 <STO>
A;Cross-references: UNIPROT:O87708; GB:AE005673; NID:g13423422; PIDN:AAK23936.1; GSPDB:G
C;Genetics:
A;Gene: CC1961
C;Superfamily: heat shock protein hslU; FtsH/SEC18/CDC48-type ATP-binding domain homolog
Query Match 25.0%; Score 5; DB 2; Length 420;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 LTTFMF 19
|||
Db 378 LTTFMF 382

Search completed: October 26, 2004, 07:23:36
Job time : 20.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 26, 2004, 06:48:06 ; Search time 91.5 Seconds
 (without alignments)
 125.765 Million cell updates/sec

Title: US-10-066-965A-3

Perfect score: 20

Sequence: 1 PRGAMNNRWVQMLETMFL 20

Scoring table: "OLIGO" Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size :

0

Total number of hits satisfying chosen parameters:

1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02:
 1: uniprot_sprot:
 2: uniprot_trembl:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Score Match Length DB ID

Result No. Description

1	6	30.0	82	2	Q8VJN1	Q8vjn1 mycobacteri
2	6	30.0	189	2	Q6VAB5	Q6vab5 trichosurus
3	6	30.0	189	2	AAO24229	Aag24229 trichosurus
4	6	30.0	192	1	DBF_THETH	pa3522 thermus the
5	6	30.0	192	2	Q72h33	Q72h33 thermus the
6	6	30.0	192	2	AASB2004	Has82004 thermus t
7	6	30.0	232	1	DEF_DEIRA	Q9rrq4 deinococcus
8	6	30.0	253	2	Q8lin8	Q8linas oryza sativa
9	6	30.0	254	2	Q83TQ5	Q83vg5 methylobaci
10	6	30.0	341	2	Q7NKH5	Q7nxh5 chromobacte
11	6	30.0	352	1	PO51_MOUSE	P02633 mus musculus
12	6	30.0	352	2	AAH58268	Aah68268 mus musculus
13	6	30.0	384	2	Q9C280	Q9c280 neurospora
14	6	30.0	411	2	Q7TIP7	Q9rrq4 deinococcus
15	6	30.0	438	2	Q8IV69	Q8iv6 homo sapien
16	6	30.0	478	2	Q6F1U1	Q6f1u1 mesoplasma
17	6	30.0	478	2	Q6MTY4	Q6mtv4 mycoplasma
18	6	30.0	478	2	CAE76902	Cae76902 mycoplasma
19	6	30.0	758	2	Q7KtB9	Q7Ktjb9 drosophil
20	6	30.0	1037	2	Q7YV13	Q7yv13 trypanosoma
21	6	30.0	1345	2	Q8A180	Q8a18 bacteroides
22	6	30.0	1437	1	VGLM_BUNGE	P12430 bunyavirus
23	6	30.0	1703	2	Q9V9A9	Q9v9a9 drosophila
24	5	25.0	23	2	Q83SX5	Q83sx5 salmonella
25	5	25.0	28	2	Q80KE5	Q80ke5 rabies virus
26	5	25.0	28	2	Q80KE7	Q80ke7 rabies virus
27	5	25.0	28	2	Q80KE9	Q80ke9 rabies virus
28	5	25.0	28	2	Q80KE0	Q80ef0 rabies virus
29	5	25.0	28	2	Q80KE2	Q80ef2 rabies virus
30	5	25.0	28	2	Q80KE3	Q80ef3 rabies virus
31	5	25.0	28	2	Q80KE4	Q80ef4 rabies virus

ALIGNMENTS

RESULT 1	Q8VJN1	PRELIMINARY;	ERT;	82 AA.	
	ID Q8VJN1_				
	AC AC				
	DT 01-MAR-2002	(TREMBLrel. 20, Created)			
	DT 01-MAR-2002	(TREMBLrel. 20, Last sequence update)			
	DE Hypothetical protein MT2341.				
	GN OrderedLocusNames=MT2341;				
	OS Mycobacterium tuberculosis.				
	OC Bacteria; Actinobacteria; Actinomycetales;				
	OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
	NCBI_TAXID=1773;				
	RN [1]				
	RP SEQUENCE FROM N.A.				
	RC STRAIN=CDC 1551 / Oshkosh;				
	RX MEDLINE=22206494; PubMed=12218036;				
	RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,				
	RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,				
	RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermlaeva M.D.,				
	RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,				
	RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,				
	RA Fraser C.M.;				
	RT "Whole genome comparison of Mycobacterium tuberculosis clinical and				
	RT laboratory strains.";				
	RL J. Bacteriol. 184:5479-5490(2002).				
	DR EBO07077; AAK46625.1; - .				
	DR TIGR; MT2341; - .				
	KW Hypothetical protein.				
	SQ SEQUENCE 82 AA; B8935 MW; C460094E66DC09E CRC64;				
	Query Match Score 6;	DB 2;	Length 82;		
	Best Local Similarity 100.0%; Pred. No. 25;				
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
	Qy 2 RGAPMW 7				
	Db 6 RGAPMW 11				
	RESULT 2				
	Q6VABS	PRELIMINARY;	PRT;	189 AA.	
	ID Q6VABS_				
	AC Q6VABS;				
	DT 05-JUL-2004	(TREMBLrel. 27, Created)			
	DT 05-JUL-2004	(TREMBLrel. 27, Last sequence update)			
	DT 05-JUL-2004	(TREMBLrel. 27, Last annotation update)			
	DE POU domain class 5 transcription factor 1-like protein				
	DE [Fragment].				
	GN Name=POU5F1;				
	OS Trichosurus vulpecula (Brush-tailed possum).				
	OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	OC NCBI_TAXID=9337;				
	RP SEQUENCE FROM N.A.				
	RA Frankenberger S., Tissell D., Selwood L.;				
	RA Submitter (JUL-2003) to the EMBL/GenBank/DBJ databases.				
	RA [1]				
	RX MEDLINE=21094456; PubMed=11170265;				
	RA Frankenberger S., Tissell D., Selwood L.;				
	RA Submitter (JUL-2003) to the EMBL/GenBank/DBJ databases.				
	RA [1]				
	RT "Identification of a homologue of POU5F1 (OCT3/4) in a marsupial, the				
	RT brushtail possum."				
	RT Mol. Reprod. Dev. 58:255-261 (2001).				
	RN [2]				
	SEQUENCE FROM N.A.				
	RA Frankenberger S., Tissell D., Selwood L.;				
	RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.				
	CC 1- SUBCELLULAR LOCATION: Nuclear (By similarity).				
	DR InterPro; IPR001356; Homeobox.				
	DR InterPro; IPR009057; Homeodomain_like.				
	DR InterPro; IPR010982; Lambda_like_DNA.				
	DR InterPro; IPR006327; POU.				
	DR InterPro; IPR007103; POU_homeo.				
	RESULT 4				
	DEF THETH 4				
	ID DEF THETH STANDARD;				
	AC P43520;				
	DT 01-NOV-1995 (Rel. 32, Created)				
	DT 01-NOV-1995 (Rel. 32, Last sequence update)				
	DT 05-JUL-2004 (Rel. 44, Last annotation update)				
	DE Peptide deformylase (EC 3.5.1.88) (PDF) (Polypeptide deformylase).				
	GN Name=def;				
	OC Thermus thermophilus.				
	OC Bacteria; Deinococcus-Thermus; Deinococci; Thermaceae.				

OC Thermus.
 OC NCBI_TaxID=274;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=VKL;
 RC MEDLINE=95050326; PubMed=7961514;
 RX RA Meimann T.; Blanquet S.;
 RA "Characterization of the *Thermus thermophilus* locus encoding peptide deformylase and methionyl tRNA(fMet) formyltransferase.",
 RL J. Bacteriol. 176:7387-7390 (1994).
 RN [2] CHARACTERIZATION.
 RP MEDLINE=97272005; PubMed=9126850;
 RX RA Meimann T.; Lazzennec C.; Villongoit S.; Blanquet S.;
 RT "Structure-function relationships within the peptide deformylase family. Evidence for a conserved architecture of the active site involving three conserved motifs and a metal ion.",
 RT J. Mol. Biol. 267:749-761 (1997).
 :- FUNCTION: Removes the formyl group from the N-terminal Met of newly synthesized proteins. Requires at least a dipeptide for an efficient rate of reaction. N-Terminal-L-methionine is a prerequisite for activity but the enzyme has broad specificity at other positions (By similarity).
 CC -!- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)O = formate + methionyl peptide.
 CC -!- COFACTOR: Binds 1 iron(II) ion (By similarity).
 CC -!- SIMILARITY: Belongs to the polypeptide deformylase family.
 CC -----
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 CC -----
 DR EMBL; X79087; CAA55695.1; -.
 DR HAMAP; MF_00163; -; 1.
 DR InterPro; IPR00181; Pmet deformylase.
 DR PRINTS; PRO1576; PDEFORMYLASE.
 DR PRODOM; PD003844; Pep_deformylase; 1.
 DR TIGRFAMS; TIGR00079; Pepf deformyl; 1.
 KW Hydrolyase; Iron; Protein biosynthesis.
 FT ACT_SITE 146 By similarity.
 FT METAL 102 Iron (By similarity).
 FT METAL 145 Iron (By similarity).
 FT METAL 149 Iron (By similarity).
 SQ SEQUENCE 192 AA; 22092 MW; 665945183A251361 CRC64;
 Query Match 30.0%; Score 6; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; MisMatches 0; OX
 Qy 14 MLETMF 19
 Db 33 MLETMF 38
 RN [1] SEQUENCE FROM N.A.
 RP PubMed=15064768;
 RX RA Henne A.; Brueggemann H.; Raasch C.; Wiezer A.; Hartsch T.; Gohl O.; Martinez-Arias R., Liesegang H.; Johann A.; Lienard T.; Gohl O.; Martinez-Arias R., Jacob C.; Starckviene V.; Schlenzcek S.; Dencker S.; Merkl R.; Goetschalk G.; Fritz H.-J.; Klens H.-P.; Kramer W.; Goetschalk G.; Fritz H.-J.; RT "The genome sequence of the extreme thermophile *Thermus thermophilus*.", Nat. Biotechnol. 22:547-553 (2004).
 CC -!- SIMILARITY: Belongs to the polypeptide deformylase family.
 DR EMBL; AE017306; AASB2004.1;
 DR GO; GO:0008463; F:formylmethionine deformylase activity; IEA.
 DR InterPro; IPR000181; F:hydrolyase activity; IEA.
 DR PF01327; Pep deformylase; 1.
 DR PRINTS; PRO1576; PDEFORMYLASE.
 DR PRODOM; PD003844; Pmet deformylase; 1.
 DR TIGRFAMS; TIGR00079; Pepf deformyl; 1.
 KW Complete proteome; Hydrolyase; Sequence 192 AA; 22092 MW; 665945183A251361 CRC64;
 Query Match 30.0%; Score 6; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; MisMatches 0; OX
 Qy 14 MLETMF 19
 Db 33 MLETMF 38
 RN [1] SEQUENCE FROM N.A.
 RP PubMed=15064768;
 RX RA Henne A.; Brueggemann H.; Raasch C.; Wiezer A.; Hartsch T.; Gohl O.; Martinez-Arias R., Liesegang H.; Johann A.; Lienard T.; Gohl O.; Martinez-Arias R., Jacob C.; Starckviene V.; Schlenzcek S.; Dencker S.; Merkl R.; Goetschalk G.; Fritz H.-J.; Klens H.-P.; Kramer W.; Goetschalk G.; Fritz H.-J.; RT "The genome sequence of the extreme thermophile *Thermus thermophilus*.", Nat. Biotechnol. 22:547-553 (2004).
 CC -!- SIMILARITY: Belongs to the polypeptide deformylase family.
 DR EMBL; AE017306; AASB2004.1;
 DR Sequence 192 AA; 22092 MW; 665945183A251361 CRC64;
 Query Match 30.0%; Score 6; DB 2; Length 192;
 Best Local Similarity 100.0%; Pred. No. 53; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; MisMatches 0; OX
 Qy 14 MLETMF 19
 Db 33 MLETMF 38
 RESULT 5
 ID Q72H33 PRELIMINARY;
 AC Q72H33; PRT; 192 AA.
 DT 05-JUL-2004 (TREMBL); 27, Created
 DT 05-JUL-2004 (TREMBL); 27, Last sequence update
 DT 05-JUL-2004 (TREMBL); 27, Last annotation update
 DE Polypeptide deformylase, fms protein-like protein (EC 3.5.1.31).
 GN OrderedLocusNames=TCI622;
 OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
 OC Bacteria; Deinococcus-Thermus; Deinococci; Thermoales; Thermaceae;
 OC Thermus.
 NCBI_TaxID=262724;

DT	01-OCT-2004 (Rel. 45, Last annotation update)	
DE	Peptidyl deformylase (EC 3.5.1.88) (PPD) (Polypeptide deformylase).	
GN	Name=def; OrderedLocusNames=DR2434;	
QS	Deinococcus radiodurans.	
OC	Bacteria; Deinococcus-thermus; Deinococci; Deinococcales;	
OC	Deinococcaceae; Deinococcus.	
OX	NCBI_TAXID=1299;	
RN	RP	SEQUENCE FROM N.A.
RC	SPRAINER1 / ATCC 13939 / DSM 20539 / NCIB 9279;	GN ORFNames=OSJUNBA0047G15.19;
RX	MEDLINE=2003:896; Published=10/07/2003;	OS Oryza sativa (Japonica cultivar-group).
RA	White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
RA	Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,	OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
RA	Moffat K.S., Qin J., Jiang L., Pamphilis W., Crosby M., Shen M.,	OC Ehrhartoides; Oryzae; Oryza.
RA	Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,	OX NCBI_TAXID=19947;
RA	Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,	RN [1]
RA	Fraser C.M.,	RP SEQUENCE FROM N.A.
RT	"Genome sequence of the radioresistant bacterium Deinococcus	RA McCombie W.R., Spiegel L., de la Bastide M., Nascimento L.,
RT	radiodurans R1." / Science 286:1571-1577 (1999).	RA Preston R., Ferraro K., Kuit K., Balija V., Bell M.,
CC	-I- FUNCTION: Removes the formyl group from the N-terminal Met of	RA Baker J., Miller B., Katzenberger F., Muller S., King L., Sullivan P.,
CC	newly synthesized proteins. Requires at least a dipeptide for an	RA Yang C., Duke S., O'Shaughnessy A., Palmer L., Dedhiu N.;
CC	efficient rate of reaction. N-terminal L-methionine is a	RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC	prerequisite for activity but the enzyme has broad specificity at	RN [2]
CC	other positions (By similarity).	RP SEQUENCE FROM N.A.
CC	-I- CATALYTIC ACTIVITY: Formyl-L-methionyl peptide + H(2)O = formate +	RA The Rice Chromosome 10 Sequencing Consortium;
CC	methionyl peptide.	RT "In-depth view of structure, activity, and evolution of rice
CC	-I- COFACTOR: Binds 1 iron(II) ion (By similarity).	RT chromosome 10";
CC	-I- SIMILARITY: Belongs to the polypeptide deformylase family.	RL Science 300:1566-1569 (2003).
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	RN [3]
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	RP SEQUENCE FROM N.A.
CC	the European Bioinformatics Institute. There are no restrictions on its	RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
CC	use by non-profit institutions as long as its content is in no way	RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
CC	modified and this statement is not removed. Usage by and for commercial	RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).	RA [4]
CC		RA [5]
DR	AB002073; AAF11975.1; -.	RESULT 9
DR	PIR: H75274; H75274.	Q83VQ5
DR	HSSP: Q91T7A8; IN5N.	ID Q83VQ5; PRELIMINARY; PRT; 254 AA.
DR	TIGR: DR2434; -.	AC Q83VQ5;
DR	HAMAP: MF_00163; -; 1.	DT 01-JUN-2003 (TRMBLrel. 24, Created)
DR	InterPro: IPR000181; Fmet_deformylase.	DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)
DR	PRINTS: PRO1576; PDEFORMYLASE.	DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DR	ProDom: PD003844; Pep_deformylase; 1.	DE EpsP.
DR	TIGRFAMS: TIGR00079; Pept_deformyl; 1.	GN Name=epSP;
KW	Complete Proteome: Hydrolase; Iron; Protein biosynthesis.	OS Methylobacillus sp. 12S.
FT	ACT SITE 179 179 By similarity.	OC Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;
FT	METAL 135 135 Iron (By similarity).	OC Methylophilaceae; Methylobacillus
FT	METAL 178 178 Iron (By similarity).	OX NCBI_TAXID=94001;
FT	METAL 182 182 Iron (By similarity).	RN [1]
SQ	SEQUENCE 232 AA; 26369 MW; 94A31686AB872ED8 CRC64;	RP SEQUENCE FROM N.A.
SQ		RC STRAIN=12S;
Query Match	Best Local Similarity 30.0%; Score 6; DB 1; Length 232;	RX MEDLINE=22511518; PubMed=12624205;
Matches	6; Conservative 100.0%; Pred. No. 63; Mismatches 0; Indels 0; Gaps 0;	RA Yoshida T., Ayabe Y., Yasunaga M., Usami Y., Habe H., Nojiri H.,
Y	14 MLETMF 19	RA Omori T.;
db	62 MLETMF 67	RT "Genes involved in the synthesis of the exopolysaccharide methanolan
RESULT 8		RT by the obligate methylotroph Methylobacillus sp. strain 12S.";
Q8LNAB	PRELIMINARY; PRT; 253 AA.	RL Microbiology 14(9):431-444 (2003).
AC	Q8LNAB; PRELIMINARY; PRT; 253 AA.	DR AB062506; BAC5144.1; -.
DT	01-OCT-2002 (TRMBLrel. 22, Created)	DR GO: GO-0009058; P:biosynthesis; IEA.
DT	01-OCT-2002 (TRMBLrel. 22, Last annotation update)	DR InterPro: IPR004629; WebC-Taga_CpsF.
DT	05-JUL-2004 (TRMBLrel. 27, Last annotation update)	DR TIGRFAMS: TIGR00696; webC-tagA_cpsF; 1.
DE	Hypothetical protein OSJUNBA0047G15.19.	SQ SEQUENCE 254 AA; 28235 MW; ABCG7E24A8BE84C3 CRC64;
Qy	4 APMMMR 9	Query Match 30.0%; Score 6; DB 2; Length 254;
AC	Q8LNAB; PRELIMINARY; PRT; 253 AA.	Best Local Similarity 100.0%; Pred. No. 68;
AC	Q8LNAB; PRELIMINARY; PRT; 253 AA.	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 209 AFMMMR 214

RESULT 10

Q7NXH5 PRELIMINARY; PRT; 341 AA.
 AC Q7NXH5;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE L-threonine 3-dehydrogenase (EC 1.1.1.103).
 GN Name=t-dih; OrderedLocusNames=CV1651;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=ATCC 1247 / DSM 30191 / PubMed=1450782;
 RX MEDLINE=22882880; PubMed=1450782;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
 RA Astolfei-Filho S., Azevedo V., Baptista A.J., Batatais L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordini J., Brígido M.M., Britto C.A., Brocchini M., Buriti H.A.,
 RA Camargo A., Cardoso D.D.P., Carneiro N.P., Carrasco D.M.,
 RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior C., Fagundes C.L.,
 RA Fantinatti F., Faria I.T.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
 RA Gazzanelli R.T., Gomes E.A., Gonçalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Gríbard E.C., Jardim S.N., Laurino J.,
 RA Leo L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
 RA Madeira F.G.P., Manfio G.P., Maranhão R., Martins W.S.,
 RA da Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixão R.F.C., Parente J.A., Pedraza F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo J.U., Rondinelli E.,
 RA Santos E.P.C., Santos F.R., Schneider D.W., Seuanes H.N.,
 RA Silva A.M.R., da Silva A.L.C., Silveira D.W., Silva R., Simões I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wasserman R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals
 RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003);
 CC [-] SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
 family.
 DR EMBL; AE016915; AAQ59327; 1; -
 DR GO; GO:004034; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
 DR GO; GO:0008743; F:L-threonine 3-dehydrogenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:008270; F:zinc ion binding; IEA.
 DR GO; GO:006567; P:threonine catabolism; IEA.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; GroES related.
 DR InterPro; IPR011597; GroES related.
 DR InterPro; IPR004627; Lthr_3_dehydrog.
 DR InterPro; IPR002025; NAD_B5.
 DR ProDom; PD040557; GroES related; 1.
 DR TIGR00690; tdh; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Complete proteome; Metal-binding; Oxidoreductase; Zinc.
 SQ SEQUENCE 341 AA;
 Query Match 30.0%; Score 6; DB 2; Length 341;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QMLETM 18
 Db 248 QMLETM 253

RESULT 11
 P051_MOUSE STANDARD; PRT; 352 AA.
 AC P051_MOUSE; STANDARD; PRT; 352 AA.
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE POU domain, class 5, transcription factor 1 (Octamer-binding
 DE transcription factor 3 (Oct-3) (Oct-4) (NF-A3);
 GN Name=douSF; Synonyms=Oct3; Octf-3, Oct-3, Oct-4;
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Vertebrata; Euteleostomi;
 OC Bokaryota; Metazoa; Chordata; Craniata; Sciuromorphata; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1] NCBI_TaxID=10090;
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90294899; PubMed=1972777;
 RA Rosner M.H., Vigano M.A., Ozato K., Timmons P.M., Poirier P.,
 RA Rigby P.W.J., Staudt L.;
 RA "A POU-domain transcription factor in early stem cells and germ cells
 RT of the mammalian embryo.";
 RL Nature 345:686-692 (1990).
 RN [2] SEQUENCE FROM N.A.
 RX MEDLINE=9006045; PubMed=1690859;
 RA Schoeler H.R., Ruppert S., Suzuki N., Chowdhury K., Grus P.;
 RA "New type of POU domain in germ line-specific protein Oct-4.";
 RL Nature 344:435-439 (1990).
 RN [3] SEQUENCE FROM N.A.
 RX MEDLINE=90150273; PubMed=1967980;
 RA Okamoto K., Okazawa H., Okuda A., Sakai M., Muramatsu M., Hamada H.;
 RA "A novel octamer binding transcription factor is differentially
 RT expressed in mouse embryonic cells.";
 RL Cell 60:461-472 (1990).
 RN [4] REVISIONS, SEQUENCE FROM N.A.
 RX MEDLINE=92007744; PubMed=915274;
 RA Okazawa H., Okamoto K., Ishino F., Ishino-Kaneko T., Takeda S.,
 RA Toyota Y., Muramatsu M., Hamada H.;
 RA "The Oct3 gene, a gene for an embryonic transcription factor, is
 RT controlled by a retinoic acid repressible enhancer.";
 RL EMBO J. 10:2997-3005 (1991).
 RN [5] STRUCTURE BY NMR OF POU DOMAIN.
 RX MEDLINE=93238934; PubMed=8097478;
 RA Morita E.H., Shirakawa M., Hayashi F., Inagawa M., Kyogoku Y.;
 RT "Secondary structure of the Oct-3 POU homeodomain as determined by 1H-
 RT 15N NMR spectroscopy.";
 RL FEBS Lett. 321:107-110 (1993).
 CC [-] FUNCTION: Transcription factor that binds to the octamer motif
 CC (5'-ATTGCAAT-3'). Prime candidate for an early developmental
 CC control gene.
 CC [-] SUBCELLULAR LOCATION: Nuclear.
 CC [-] SIMILARITY: Belongs to the POU transcription factor family. Class-
 CC 5 subfamily.
 CC [-] SIMILARITY: Contains 1 homeobox domain.
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 CC
 DR EMBL; M34381; AAA39844.1; ALT_SEQ.
 DR EMBL; X52437; CAA36682.1; -.

DR	EMBL; S58426; AAB19896-1; -.	RA	Diarchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Botaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Richards S., Worley S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Hellton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M., Butterfield Y.S., Kryzwienski M.I., Skalska U., Smaitius D.E., Schnurch A., Schein J.E., Jones S.J., Marra M.A.; Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;	RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
DR	EMBL; S58422; AAB19896-1; JOINED.	RA	Strain=CS7BL/6J; TISSUE=Embryo; STRAIN=CS7BL/6J; TISSUE=Embryo;	RP	SEQUENCE FROM N.A.
DR	EMBL; S58423; AAB19896-1; JOINED.	RA	Strausberg R.; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	RC	STRAIN=CS7BL/6J; TISSUE=Embryo;
DR	EMBL; S58424; AAB19896-1; JOINED.	RA	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	RL	Strausberg R.; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; S58425; AAB19896-1; JOINED.	RA	EMBL; BC068268; AA668268; 1; -.	RQ	SEQUENCE FROM N.A.
PIR	PIR: A34672; A34672.	RA	Hypothetical protein.	RQ	SEQUENCE FROM N.A.
DR	PIR; S17313; S17313.	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
PDB	1OCP; NMR; @=216-282.	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
TRANSPC	T00651; -.	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
DR	MGD; MGI:101893; Pou5f1.	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
DR	GO; GO:000634; C:nucleus; IC.	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
DR	GO; GO:0003700; P:transcription factor activity; IDA.	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
DR	GO; GO:0006366; P:transcription from Pol II promoter; IDA.	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
DR	InterPro; IPR001356; Homeobox.	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
DR	InterPro; IPR009457; Homeodomain_like.	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
DR	InterPro; IPR010982; Lambda-like_DNA.	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
DR	InterPro; IPR000327; POU.	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
DR	InterPro; IPR007103; POU_homeo.	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
PFam	PF00046; Homeobox; 1.	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
DR	PFam; PF00157; Pou; 1.	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
PRINTS	PR00024; HOMEBOX.	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
DR	PRINTS; PR00028; POUDOMAIN.	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
DR	ProDom; P000010; Homeobox; 1.	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
DR	ProDom; PD000583; pou_domain; 1.	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
SMART	SM00389; HOX; 1.	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
DR	SMART; SM00352; pou; 1.	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
DR	PROSITE; PS0027; HOMEBOX_1; 1.	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
DR	PROSITE; PS50071; HOMEBOX_2; 1.	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
DR	PROSITE; PS50035; POU_1; 1.	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
DR	PROSITE; PS00465; POU_2; 1.	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
KW	3D-structure; DNA-binding; Homeobox; Nuclear protein;	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
KW	Transcription regulation.	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DOMAIN 135 205	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
DNA BIND	223 282	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 242	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	HELIX 250 260	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	TURN 261 261	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 264 275	RA	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RQ	SEQUENCE FROM N.A.
FT	DE 275 275	RA	KW Hypothetical protein.	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 28	RA	SEQUENCE 352 AA; 38216 MW; 757B41DF52286714 CRC64;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 1 29	RA	Query Match Score 6; DB 2; Length 352;	RQ	SEQUENCE FROM N.A.
FT	CONFICT 31 31	RA	Best Local Similarity 100.0%; Pred. No. 91;	RQ	SEQUENCE FROM N.A.
FT	HELIX 232 2				

AC	Q871P7;	[2]	RN	SEQUENCE FROM N.A.
DT	01-JUN-2003 (TREMBLrel. 24, Created)	RP	RC	TISSUE=Brain;
DT	01-OCT-2003 (TREMBLrel. 24, Last sequence update)	RA	Strausberg R.;	
DE	Hypothetical protein VPA0559.	RA	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.	
GN	OrderedLocusNames=VPA0559;	RL	EMBL: BC042452; AAH42452.1; -;	
OS	Vibrio parahaemolyticus.	DR	GO; GO:0016021; C:integral to membrane; IEA.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;	DR	GO; GO:0005215; F:transporter activity; IEA.	
OC	Vibrionaceae; Vibrio.	DR	GO; GO:006810; P:transport; IEA.	
NCBI_TAXID=670;	OX	DR	GO; GO:001114; MFS.	
RN	[1] —	DR	InterPro; IPR001114; MFS.	
RP	SEQUENCE FROM N.A.	DR	InterPro; IPR004156; OATP_Cterm.	
RC	STRAIN=RIMD 210633 / Serotype 03:K6;	DR	InterPro; IPR004156; OATP_Nterm.	
RX	REMLINE 210633; PubMed=02620739;	DR	pfam; PF03137; CATP; 1.	
RA	Makino K., Oshima K., Kurokawa K., Yokoyama K., Iida T., Tagomori K.,	DR	TIGRFAMS; TIGR0085; oat; 1.	
RA	Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,	FT	PROSITE; PS5085; MFS; 1.	
RA	Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;	FT	NON_TIR; 1	
RT	"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."	SEQUENCE	438 AA; 49086 MW; 8367CC253A77D433 CRC64;	
RT	Lancet 361:743-749 (2003).	Qy	15 LETMFL 20	
RL	AP005085; BAC67902.1; -;	Db	28 LETMFL 33	
DR	DR; GO:0016020; C:membrane; IEA.	RESULTS 16	Query Match 30.0%; Score 6; DB 2; Length 438;	
DR	InterPro; IPR004838; DUF244.	ID	Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;	
DR	Pfam; PF02287; FtsX; 1.	Q6F1U1	Score 6; DB 2; Length 438;	
KW	Complete proteome; Hypothetical protein.	PRELIMINARY;	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
SQ	SEQUENCE 411 AA; 45224 MW; 99CB9E2E7E7AD331 CRC64;	AC	Score 6; DB 2; Length 438;	
Qy	15 LETMFL 20	DT	Created) 01-OCT-2004 (TREMBLrel. 28, Last sequence update)	
Db	320 LETMFL 325	DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)	
RESULTS 17	OS	DE	Pyruvate kinase;	
Q8IV69	PRELIMINARY;	GN	ORFNAMES=MF1175;	
ID	Q8IV69;	OS	Mesoplasma florum Ll.	
AC	OBIV69;	OC	Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;	
DT	01-MAR-2003 (TREMBLrel. 23, Created)	OC	Entomoplasmataceae; Mesoplasma.	
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	RN	NCBI_TAXID=65311;	
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	[1]	RN	
DB	SLCO1A2 protein (Fragment).	RP	SEQUENCE FROM N.A.	
GN	Name=SLCO1A2;	RC	STRAIN=L1;	
OS	Homo sapiens (Human).	RA	Birren B.W.; Stange-Thomann N., Hafetz N., DeCaprio D., Fisher S.,	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RA	Major J., Wang S., Nicol R.,	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	RA	Butler J., Elkins T., Kodra C.D., Major J., Wang S., Nicol R.,	
NCBI_TAXID=9606;	RN	[2]	Nusbam C.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases	
RN	SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.A.	
RC	TISSUE=Brain.	RA	RN	
RX	MEDLINE 22388257; PubMed=12477932;	RA	Knight T. Jr., Fournier G.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	DR	DR	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schulter G.D.,	AE017263; AAT75532.1; -.		
RA	Altschul S.F., Zeeberg B., Butow K.H., Schaefer C.F., Bhat N.K.,	KW	Kinase; Pyruvate;	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	SEQUENCE	478 AA; 53085 MW; DEF903F6A09938DD CRC64;	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	Query Match 30.0%; Score 6; DB 2; Length 478;		
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;		
RA	Raha S.S., Loqueland N.A., Peters G.J., Carninci P., Prange C.,	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
RA	Bosek S.A., McEwan P.J., Abramson R.D., Mullally S.J.,	Qy	13 QMLETM 18	
RA	Richards S., Worley K.C., McKernan K.J., Malek J.A., Garcia A.M., Gay L.J., Huiyk S.W.,	Db	290 QMLETM 295	
RA	Villalon D.K., Muñoz D.M., Sodergren E.J., Lu X., Gibbs R.A.,	RESULTS 17	RESULTS 17	
RA	Fahy J., Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,	Q6MTY4	Q6MTY4; PRELIMINARY;	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	AC	Q6MTY4; PRELIMINARY;	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	DT	05-JUL-2004 (TREMBLrel. 27, Created)	
RA	Rodriguez A.C., Grimwood J., Schmutz J.W., Myers R.M., Butterfield Y.S.,	DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	
RA	Kirzynski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.E.,	DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human	RL	Pyruvate kinase (EC 2.7.1.40).	
RT	and mouse cDNA sequences.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			

GN	Name=DYK; OrderedLocusNames=MSC_0261;
OS	Mycoplasma mycooides (subsp. mycooides SC).
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX	NCBI_TaxID=44101;
RN	[1] SEQUENCE FROM N.A.
RC	STRAIN=PGI;
RX	PubMed-14762060;
RA	Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycooides subsp. mycooides SC type strain PG1T, the causative agent of contagious bovine pleuropneumonia (CBPP)." Genome Res. 14:221-227 (2004).
RT	-!- CATALYTIC ACTIVITY: ATP + Pyruvate = ADP + phosphoenolpyruvate.
CC	CC -!- COFACTOR: Requires magnesium and potassium (By similarity).
CC	CC -!- PATHWAY: Glycolysis; final step.
CC	CC -!- SUBUNIT: Homotetramer. Belongs to the pyruvate kinase family.
DR	EMBL: BX82642; CAE6902.1; GO: GO:0004743; P:Pyruvate kinase activity; IEA.
DR	GO: GO:0016740; P:Transf erase activity; IEA.
DR	InterPro: IPR001697; Pyruvate_kinase.
DR	Pfam: PF00224; PRK_1.
DR	PRINTS: PRO01050; PYRUVATKNASE.
DR	ProDom: PDO01009; Pyruvate kinase; 2.
DR	TIGRFAMS: TIGR01064; pyruv_kin_1.
KW	Complete proteome; Glycolysis; Kinase; Magnesium; Pyruvate;
SEQUENCE	478 AA; 53817 MW; 1CE5709BA6305C9 CRC64;
SQ	Query Match 30.0%; Score 6; DB 2; Length 478; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	13 QMLETM 18
Db	290 QMLETM 540
RESULT 19	
Q7KJB9	PRELIMINARY; PRT; 758 AA.
ID	Q7KJB9
AC	Q7KJB9;
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	DE L(2) 01289 Long form (Fragment).
GN	GN Name=DYK; 01289;
OS	Drosophila melanogaster (Fruit fly)
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila.
OC	NCBI_TaxID=7227;
OX	OX RN
RP	SEQUENCE FROM N.A.
RA	Manning G., Micklem D.R., Krasnow M.A.; Manning G., Micklem D.R., Krasnow M.A.; Submitted (DBC-1999) to the EMBL/GenBank/DDBJ databases.
RL	DR EMBL: AF216976; AAC34750.1; -
DR	InterPro: IPR006663; Thioredox_dom2.
FT	NON_TER 1 1
FT	NON_TER 758 758
SQ	SEQUENCE 758 AA; 88075 MW; CB31F4196C4BA315 CRC64;
Query Match 30.0%; Score 6; DB 2; Length 758; Best Local Similarity 100.0%; Pred. No. 1.8e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	13 QMLETM 18
Db	535 QMLETM 540
RESULT 20	
Q7YV13	PRELIMINARY; PRT; 1037 AA.
ID	Q7YV13
AC	Q7YV13;
DT	01-OCT-2003 (TREMBLrel. 25, Created)
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	DE Protein kinase, putative.
GN	GN ORFName=TR97_2.4200;
OS	OS Trypanosoma brucei.
OC	OC NCBI_TaxID=5691;
RN	RN SEQUENCE FROM N.A.
RP	RP SEQUENCE FROM N.A.
RX	RX MEDLINE=22789168; PubMed=12907728;
RA	RA Bl-Sayed N.M.A.; Ghedin E.; Song J.; MacLeod A.; Bringaud F.; Larkin C.; Wanless D.; Peterson J.; Hou L.; Taylor S.; Tweedie A.; Bitteau N.; Khalak H.G.; Lin X.; Mason T.; Hamnic L.; Caler E.; Blandin G.; Bartholomeu D.; Sampson A.J.; Raul S.; Zhao H.; Pai G.; Van Aken S.; Utterback T.; Haas B.; Koo H.L.; Umayam L.; Gerard C.; Leech V.; Oi R.; Zhou S.; Schwartz D.; Feldblum T.; Salzberg S.; Tait A.; Turner M.R.; Ullil E.; White O.; Melville S.; Adams M.D.; Fraser C.M.; Donelson J.E.;
RA	RA RT "The sequence and analysis of trypanosoma brucei chromosome II." Nucleic Acids Res. 31:4855-4863 (2003).
RL	RL -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC	CC EMBL: AE017169; AAQ15877.1; -
DR	DR GO; GO:0005524; F:ATP binding; IEA.
DR	DR GO; GO:0004674; F:serine/threonine kinase activity; IEA.
DR	DR GO; GO:0016740; F:Transferase activity; IEA.
DR	DR InterPro: IPR0082271; Ser_Thr_pkin_AS.
DR	DR ProDom; PD00001; Prot kinase 1.
DR	DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR	DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR	DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Qy	13 QMLETM 18
Db	290 QMLETM 295
RESULT 18	
C2E76902	PRELIMINARY; PRT; 478 AA.
AC	CAE76902;
DT	02-MAR-2004 (TREMBLrel. 27, Created)
DT	13-APR-2004 (TREMBLrel. 27, Last sequence update)
DE	DE Pyruvate kinase (EC 2.7.1.40).
OS	OS Mycoplasma mycooides (subsp. mycooides SC).
OC	OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=44101;	RN [1] SEQUENCE FROM N.A.
RC	STRAIN=PGI;
RX	PubMed-14762060;
RA	Westberg J., Persson A., Holmberg A., Goesmann A., Lundeberg J., Johansson K.-E., Pettersson B., Uhlen M.; "The genome sequence of Mycoplasma mycooides subsp. mycooides SC type strain PG1T, the causative agent of contagious bovine pleuropneumonia (CBPP)." Genome Res. 14:221-227 (2004).
RT	RT Kinase; Pyruvate; Transferase.
RT	RT Scores 30.0%.
RL	RL Kinase; Pyruvate; Transferase; Pyruv_kin_1.
SQ	SQ Query Match 30.0%; Score 6; DB 2; Length 478; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	13 QMLETM 18
Db	290 QMLETM 295

KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.	Query Match Score 30.0%; Best Local Similarity 100.0%; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 30.0%; Best Local Similarity 100.0%; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
SQ	SEQUENCE 1037 AA; 113326 MW; A87B8C4442743274 CRC64;		
Query Match Score 6; DB 2; Length 1037; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 11 VCOMLE 16 Db 85 VCOMLE 90	Qy 11 VCOMLE 16 Db 1202 VCOMLE 1207	
		RESULT 22	
		ID VGLM_BUNGE STANDARD; PRT; 1437 AA.	
		AC P12430;	
		DT 01-OCT-1989 (Rel. 12, Created)	
		DT 01-OCT-1989 (Rel. 12, Last sequence update)	
		DI 05-JUL-2004 (Rel. 44, Last annotation update)	
		DE M polypeptide precursor [Contains: Glycoprotein G2; Nonstructural protein NS-M; Glycoprotein G1].	
		DE Name=M;	
		OS Bunyavirus germiston.	
		OC Virus: ssRNA negative-strand viruses; Bunyaviridae; Orthobunyavirus.	
		OX NCBI_TAXID=11574;	
		RN SEQUENCE FROM N.A.	
		RX MEDLINE=89021381; PubMed=3176688;	
		RA Pardigon N., Vialat P., Gerbaud S., Girard M.; Bouloy M.; comparison of the M gene product of several bunyaviruses.",	
		RT "Nucleotide sequence of the M segment of Germiston virus; comparison of the M gene product of several bunyaviruses.",	
		RL Virus Res. 11:73-85 (1988).	
		CC -I- PM: Specific enzymatic cleavages yield mature proteins including nonstructural protein NS-M, Glycoprotein G1, and Glycoprotein G2.	
		CC -I- SIMILARITY: Belongs to the orthobunyaviruses M polyprotein family.	
		CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
		CC EMBL; M21951; AA42778.1; -	
		DR PIR; S07430; S07430.	
		DR InterPro; IPR005167; Bunya_G1.	
		DR InterPro; IPR005168; Bunya_G2.	
		DR PFAM; PF03557; Bunya_G1; 1.	
		DR PFAM; PF03563; Bunya_G2; 1.	
		KW Glycoprotein; Nonstructural protein; Polyprotein; Signal; Transmembrane.	
		CC SIGNAL 1 21 M polyprotein.	
		FT CHAIN 22 1437 Glycoprotein G2.	
		FT CHAIN 307 481 Nonstructural protein NS-M.	
		FT CHAIN 482 1437 Glycoprotein G1.	
		FT TRANSMEM 208 228 Potential.	
		FT TRANSMEM 316 336 Potential.	
		FT TRANSMEM 368 388 Potential.	
		FT TRANSMEM 1395 1415 Potential.	
		FT CARBOHYD 65 65 N-linked (GlcNAc . .) (Potential).	
		FT CARBOHYD 88 88 N-linked (GlcNAc . .) (Potential).	
		FT CARBOHYD 252 252 N-linked (GlcNAc . .) (Potential).	
		FT CARBOHYD 474 474 N-linked (GlcNAc . .) (Potential).	
		FT CARBOHYD 627 627 N-linked (GlcNAc . .) (Potential).	
		FT CARBOHYD 1173 1173 N-linked (GlcNAc . .) (Potential).	
		SQ SEQUENCE 1437 AA; C4FB3001BD0930D CRC64;	
		Query Match Score 30.0%; Best Local Similarity 100.0%; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		DR PROSITE; PS050109; HIS_KIN; 1.	
		DR PROSITE; PS050110; HTH_ARAC_FAMILY_2; 1.	
		DR PROSITE; PS050112; HTH_ARAC; 1.	
		DR PROSITE; PS050114; HTH_ARAC; 1.	
		DR SMART; SMM0342; RBC; 1.	
		DR SMART; SMM0448; RBC; 1.	
		DR PROSITE; PS0501124; HTH_ARAC_FAMILY_2; 1.	
		DR PROSITE; PS0501124; HTH_ARAC; 1.	
		KW Complete proteome; DNA-binding; Kinase; Phosphorylation; Transferase.	
		SEQUENCE 1345 AA; 155269 MW; 7247DDA9CFADAB CRC64;	
SQ		Qy 15 LETMFL 20 Db 560 LETMFL 565	

[4]	RN	SEQUENCE FROM N.A.
	RX	MEDLINE=2246070; PubMed=12537573;
	RA	Kaminker J.S./, Bergman C.M./, Kronmiller B./, Carlson J.W./, Svirskas R./,
	RA	Ovsvag Q.V./, Patel S./, Frise E./, Wheeler D.A./, Lewis S.E./, Rubin G.M./,
	AC	Ashburner M./, Celinker S.E./, "The transposable elements of the <i>Drosophila melanogaster</i> euchromatin: a genomics perspective";
	AC	Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
	RN	[5]
	RP	SEQUENCE FROM N.A.
	RX	MEDLINE=22426059; PubMed=12537572;
	RA	Misra S./, Crosby M.A./, Mangali C.J./, Campbell K.S./, Matthews B.B./, Campbell K.S./,
	RA	Hradecky P./, Huang Y./, Kaminker J.S./, Millburn G.H./, Prochnik S.E./,
	RA	Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
	RA	Oxypodidae; Drosophilidae; Drosophila.
	OX	NCBI-TAXID=7227;
	RN	[1]
	RP	SEQUENCE FROM N.A.
	RX	Manning G./, Micklem D.R./, Krashow M.A./;
	RP	Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
	RN	[2]
	RP	SEQUENCE FROM N.A.
	RX	MEDLINE=20196006; PubMed=10731132;
	RA	Adams M.D./, Celinker S.E./, Holt R.A./, Evans C.A./, Gocayne J.D./, Amanatides P.G./, Scheer S.E./, Li P.W./, Hoskins R.A./, Galle R.F./, George R.A./, Lewis S.E./, Richards S./, Ashburner M./, Henderson S.N./, Sutton G.G./, Wortman J.R./, Yandell M.D./, Zhang Q./, Chen L.X./, Brandon R.C./, Rogers Y.H./, Blazej R.G./, Chizhik S./, Pfeiffer B.D./, Wan K.H./, Doyle C./, Baxter E.G./, Heitl G./, Nelson C.R./, Gabor G.L./, Abril J.F./, Agbayani A./, An H.U./, Andrews P./, Frankino C./, Baldwin D./, Ballieu R.M./, Basu A./, Baxendale J./, Bayraktaroglu L./, Besley E.M./, Beeson K.Y./, Benos P.V./, Berman B.P./, Bhandaari D./, Bolshakov S./, Borkovska D./, Botchan M.R./, Bouck P./, Broctier P./, Burtis K.C./, Busam D.A./, Butler H./, Cadieu E./, Center A./, Chandra I./, Cherry J.M./, Cowley S./, Dahlke C./, Davenport L.B./, Davies P./, de Pablo J./, Delcher A./, Della P./, Deyo A.D./, Dew T./, Dietz S.M./, Dodson K./, Doupe L.E./, Downes M./, Dugan-Rocha S./, Dunkov B.C./, Dunn P./, Durbin K.J./, Evangelista C.C./, Ferraz C./, Ferreira S./, Fleischmann W./, Fosler C./, Gabrieli A.E./, Garg N.S./, Gelbart W.M./, Glasser K./, Glodek A./, Gong F./, Gorrell J.H./, Gu Z./, Guan F./, Harris M./, Harris N.L./, Harvey D./, Heiman T.J.R./, Hernandez J.R./, Houck J./, Hostin D./, Houska K.A./, Howland T.J./, Ibegwam C./, Jalali M./, Kalush F./, Karpen G.H./, Ke Z./, Kennison J.A./, Ketchum K.A./, Kimmel B.E./, Kodira C.D./, Kraft C./, Kravitz S./, Kulp D./, Lai Z./, Lasko P./, Lei Y./, Levitt A.A./, Li J./, Li Z./, Liang Y./, Lin X./, Liu X./, Mattei B./, McIntosh T.C./, McLeod M.P./, McPherson D./, Merkulov G./, Milashina N.V./, Mobarry C./, Morris J./, Moshrefi A./, Mount S.M./, Moy M./, Murphy L./, Muzny D.M./, Nelson D.L./, Nelson D.R./, Nelson K.A./, Nixon K./, Nusslein D.R./, Paclob J.M./, Palazzolo M./, Pittman G.S./, Pan S./, Pollard J./, Puri V./, Reese M.G./, Reinert K./, Remington K./, Saunders R.D./, Scheier P./, Shen H./, Shue B.C./, Sinden-Kianos I./, Simpson M./, Skupski M.P./, Smith T./, Spier E./, Spradling A.C./, Stapleton M./, Strong R./, Sun E./, Svirskas R./, Tector E./, Turner E./, Wang A.H./, Wang X./, Wang Z.Y./, Wasserman D.A./, Weinstock G.M./, Weissbach J./, Williams S.M./, Woodgett J./, Worley K.C./, Wu D./, Yang S./, Yao Q.A./, Ye J./, Yeh R.F./, Zaveri J.S./, Zhan M./, Zhang G./, Zhao Q./, Zheng L./, Zheng X.H./, Zhong F.N./, Zhong W./, Zhu X./, Zhu S./, Smith H.O./, Gibbs R.A./, Myers E.W./, Rubin G.M./, Venter J.C./, "Finishing a whole-genome shotgun: release 3 of the <i>Drosophila melanogaster</i> euchromatic genome sequence";
	RT	Science 287:2185-2195(2000).
	RN	[3]
	SEQUENCE FROM N.A.	
	RX	MEDLINE=22426057; PubMed=12537568;
	RA	Celinker S.E./, Wheeler D.A./, Kronmiller B./, Carlson J.W./, Halpern A./, Patel S./, Adams M./, Champe M./, Dugan S.P./, Frise E./, Hodgeson A./, George R.A./, Hoskins R.A./, Laverty T./, Muzny D.M./, Nelson C.R./, Paclob J.M./, Park S./, Pfeiffer B.D./, Richards S./, Sodergren E.J./, Svirskas R./, Tabor P.E./, Wan K./, Stapleton M./, Sutton G.G./, Venter C./, Weinstock G./, Scherzer S.E./, Myers E.W./, Gibbs R.A./, Rubin G.M./, "Finishing a whole-genome shotgun: release 3 of the <i>Drosophila melanogaster</i> euchromatic genome sequence";
	RT	Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
	RT	Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
	RN	[6]
	SEQUENCE FROM N.A.	
	RP	FLYBASE;
	RG	Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
	RL	[7]
	RN	SEQUENCE FROM N.A.
	RP	FLYBASE;
	RG	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
	RL	EMBL; AF216973; AA34746.1; -.
	DR	EMBL; AE013790; AAN16126.1; -.
	HSPP	Q57155; 1FO5.
	DR	IntAct; Q9V9A9; -.
	DR	FBgn0010482; 1(2)01289.
	DR	Go; GO:0005489; P:electron transporter activity; IEA.
	DR	Go; GO:0006118; P:electron transport; IEA.
	DR	InterPro; IPR006662; thioired.
	DR	InterPro; IPR006663; thioredox dom2.
	DR	Pfam; PF00085; Thioredoxin; 8.
	KW	Redox-active center.
	SQ	SEQUENCE 1703 AA; 196579 MW; DAA9C246342ABDA CRC64;
	Query Match	30.0%; Score 6; DB 2; Length 1703;
	Best Local Similarity	100.0%; Pred. No. 3-6e-02;
	Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	QY	13 QMLETM 18
	Db	1348 QMLETM 1353
	RESULT 24	
	Q83SX5	PRELIMINARY; PRT; 23 AA.
	ID	SEQUENCE FROM N.A.
	AC	Q83SX5;
	DT	01-JUN-2003 (TREMBLrel. 24, Created)
	DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
	DE	Hypothetical protein.
	GN	OrderedLocusNames=L2947;
	OS	Salmonella typhi.
	OC	Enterobacteriaceae; Salmonella; Enterobacteriales;
	NCBI_TaxID=601;	
	RN	[1]
	SEQUENCE FROM N.A.	
	RP	STRAIN=TY2 / ATCC 700931;
	RC	MEDLINE=22531367; PubMed=1264504;
	RX	Deng W./, Liou S.-R./, Plunkett G.F.III., Mayhew G.F./, Rose D.J./, Burland V./, Kodoyiannii V./, Schwartz D.C./, Blattner F.R./, Comparative genomics of <i>Salmonella enterica</i> serovar <i>Typhi</i> strains Ty2 and CT18.";

RL J. Bacteriol. 185:2330-2337 (2003).
 DR EMBL; AE01644; AA070500.1; -.
 KW Hypothetical protein
 SQ SEQUENCE 23 AA; 2797 MW; 9EEB0BCB88CB36AA CRC64;

Query Match 25.0%; Score 5; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; PRT; 28 AA.

Qy 11 VCOML 1.5
 Db 16 VCOML 20

RESULTS 25
 Q80KES PRELIMINARY; PRT; 28 AA.
 AC Q80KES;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssaviruses.
 OC Rabies virus.
 OC Rhabdoviridae; Lyssavirus.
 OC Rabies virus.
 RN (1) - TAXID=11292;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Boshell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RT human and dog rabies associated with bats.;
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192397; AA045872.1; -.
 FT NON TER 28 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; PRT; 28 AA.

Qy 1 PRGAP 5
 Db 21 PRGAP 25

RESULTS 26
 Q80KET PRELIMINARY; PRT; 28 AA.
 AC Q80KET;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 OC Rabies virus.
 OC Rhabdoviridae; Lyssavirus.
 OC Rabies virus.
 RN (1) - TAXID=11292;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Bosshell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RT human and dog rabies associated with bats.;
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192397; AA045867.1; -.
 FT NON TER 28 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 21 PRGAP 25

RESULTS 29
 Q80KF2 PRELIMINARY; PRT; 28 AA.
 AC Q80KF2;

DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 NCBI_TaxID=11292;
 RN [1] _SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Boschell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats."
 RT J. Gen. Virol. 84:795-802(2003).
 RL EMBL; AY192388; AAO45864.1.; -.
 DR EMBL; AY192388; AAO45864.1.; -.
 FT NON-TER 28 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;
 Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 21 PRGAP 25

RESULT 32
 Q80KF5 PRELIMINARY; PRT; 28 AA.
 ID Q80KF5 PRELIMINARY;
 AC Q80KF5;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 NCBI_TaxID=11292;
 RN [1] _SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Boschell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats."
 RT J. Gen. Virol. 84:795-802(2003).
 RL EMBL; AY192388; AAO45864.1.; -.
 DR EMBL; AY192388; AAO45864.1.; -.
 FT NON-TER 28 SQ SEQUENCE 28 AA; 2938 MW; 2B2237A9ABBF3C6A CRC64;
 Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 21 PRGAP 25

RESULT 33
 Q80KF6 PRELIMINARY; PRT; 28 AA.
 ID Q80KF6 PRELIMINARY;
 AC Q80KF6;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 NCBI_TaxID=11292;
 RN [1] _SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Boschell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats."
 RT J. Gen. Virol. 84:795-802(2003).
 RL EMBL; AY192386; AAO45861.1.; -.
 DR EMBL; AY192386; AAO45861.1.; -.
 FT NON-TER 28 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

RESULT 31
 Q80KF4 PRELIMINARY; PRT; 28 AA.
 ID Q80KF4 PRELIMINARY;
 AC Q80KF4;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 NCBI_TaxID=11292;
 RN [1] _

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 34
Q80KF8 PRELIMINARY; PRT; 28 AA.
ID Q80KF8
AC Q80KF8;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB L_protein (Fragment).
OS Rabies virus.
OC ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
RN SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RT human and dog rabies associated with bats.;
RL Gen. Virol. 84:795-802(2003).
DR EMBL; AY192384; AAO45859.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3010 MW;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 35
Q80KF9 PRELIMINARY; PRT; 28 AA.
ID Q80KF9
AC Q80KF9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB L_protein (Fragment).
OS Rabies virus.
OC ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
RN SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Bosshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RT human and dog rabies associated with bats.;
RL Gen. Virol. 84:795-802(2003).
DR EMBL; AY192384; AAO45859.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3010 MW;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 36
Q80KG1 PRELIMINARY; PRT; 28 AA.
ID Q80KG1
AC Q80KG1;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB L_protein (Fragment).
OS Rabies virus.
OC ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;
RN SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Bosshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
human and dog rabies associated with bats.";
RT human and dog rabies associated with bats.;
RL Gen. Virol. 84:795-802(2003).
DR EMBL; AY192384; AAO45859.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3010 MW;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 21 PRGAP 25

OS Rabies virus; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Ilyssavirus.
 RN [1] _TAXID=11292;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Boschell J.;
 "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RT human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802 (2003).
 DR EMBL; AY192379; AAO45054.1; -.
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 |||||
 Db 21 PRGAP 25

RESULT 39
 Q80KG4
 ID Q80KG4 PRELIMINARY; PRT; 28 AA.
 AC DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC Rhabdoviridae; Ilyssavirus.
 RN [1] _TAXID=11292;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Boschell J.;
 "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RT human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802 (2003).
 DR EMBL; AY192378; AAO45053.1; -.
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 |||||
 Db 21 PRGAP 25

RESULT 40
 Q80KG7
 ID Q80KG7 PRELIMINARY; PRT; 28 AA.
 AC DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC Rhabdoviridae; Ilyssavirus.
 RN [1] _TAXID=11292;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A.; Nunez C.; Garcia C.; Boschell J.;
 "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RT human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802 (2003).
 DR EMBL; AY192373; AAO45054.1; -.
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RN [1]	SEQUENCE FROM N.A.		SQ	SEQUENCE	28 AA;	3010 MW;	2B3637A9AAC3C6A CRC64;
RP MEDLINE=22541850; PubMed=12655080;				Query Match	25.0%;	Score 5;	DB 2;
RA Paez A., Nunez C., Garcia C., Boschell J.;				Best Local Similarity	100.0%;	Pred. No. 1.4e+02;	Length 28;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";				Matches 5;	Conservative 0;	Mismatches 0;	Indels 0;
RL J. Gen. Virol. 84:795-802(2003).				Qy 1 PRGAP 5			Gaps 0;
DR EMBL; AY192410; AA031965.1; -.				Db 21 PRGAP 25			
FT NON_TER 28							
SQ SEQUENCE 28 AA; 2996 MW; 2B7337A9AAC3C6A CRC64;							
				RESULT 50			
				Q80KK6			
				ID Q80KK6	PRELIMINARY;		
				AC Q80KK6;			
				DT 01-JUN-2003 (TrEMBLrel. 24, Created)			
				DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
				DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
				DE L Protein (Fragment).			
				OS Rabies virus.			
				OC Viruses; ssRNA negative-strand viruses; Mononegavirales;			
				OC Rhabdoviridae; Lyssavirus.			
				OX NCBI_TaxID=11292;			
				RN [1]			
				SEQUENCE FROM N.A.			
				RP MEDLINE=22541850; PubMed=12655080;			
				RA Paez A., Nunez C., Garcia C., Boschell J.;			
				RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";			
				RL J. Gen. Virol. 84:795-802(2003).			
				DR EMBL; AY192408; AA031963.1; -.			
				FT NON_TER 28			
				SQ SEQUENCE 28 AA; 3010 MW; 2B3637A9AAC3C6A CRC64;			
				RESULT 51			
				Q80KK7			
				ID Q80KK7	PRELIMINARY;		
				AC Q80KK7;			
				DT 01-JUN-2003 (TrEMBLrel. 24, Created)			
				DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
				DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
				DE L Protein (Fragment).			
				OS Rabies virus.			
				OC Viruses; ssRNA negative-strand viruses; Mononegavirales;			
				OC Rhabdoviridae; Lyssavirus.			
				OX NCBI_TaxID=11292;			
				RN [1]			
				SEQUENCE FROM N.A.			
				RP MEDLINE=22541850; PubMed=12655080;			
				RA Paez A., Nunez C., Garcia C., Boschell J.;			
				RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";			
				RL J. Gen. Virol. 84:795-802(2003).			
				DR EMBL; AY192407; AA031962.1; -.			
				FT NON_TER 28			
				SQ SEQUENCE 28 AA; 3010 MW; 2B3637A9AAC3C6A CRC64;			
				RESULT 49			
				Q80KK5			
				ID Q80KK5	PRELIMINARY;		
				AC Q80KK5;			
				DT 01-JUN-2003 (TrEMBLrel. 24, Created)			
				DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)			
				DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
				DE L Protein (Fragment).			
				OS Rabies virus.			
				OC Viruses; ssRNA negative-strand viruses; Mononegavirales;			
				OC Rhabdoviridae; Lyssavirus.			
				OX NCBI_TaxID=11292;			
				RN [1]			
				SEQUENCE FROM N.A.			
				RP MEDLINE=22541850; PubMed=12655080;			
				RA Paez A., Nunez C., Garcia C., Boschell J.;			
				RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";			
				RL J. Gen. Virol. 84:795-802(2003).			
				DR EMBL; AY192409; AA031964.1; -.			
				FT NON_TER 28			

RESULT 52
Q8OKK8
 ID Q8OKK8; PRELIMINARY;
 AC Q8OKK8;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 NCBI_TaxID=11292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A., Nunez C., Garcia C., Boshell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
 RT RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192405; AAO31959.1; -.
 FT NON TER 28 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

RESULT 53
Q8OKK9
 ID Q8OKK9; PRELIMINARY;
 AC Q8OKK9;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 NCBI_TaxID=11292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A., Nunez C., Garcia C., Boshell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
 RT RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192403; AAO31958.1; -.
 FT NON TER 28 28
 SQ SEQUENCE 28 AA; 2938 MW; 2F733543AACAA3C6A CRC64;

RESULT 54
Q8OKL0
 ID Q8OKL0; PRELIMINARY;
 AC Q8OKL0;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

RT "Molecular epidemiology of rabies associated with bats.";
 RT human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192402; AAO31957.1; -.

FT 28
 SQ SEQUENCE 28 AA; 3010 MW; 2B3637A9AACAA3C6A CRC64;

Query Match Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PRT; 28 AA.
 PRGAP 5
 PRGAP 25

RESULT 57
 Q8OKL3 PRELIMINARY;
 ID Q8OKL3
 AC Q8OKL3;
 DT 01-JUN-2003 (TRNMBLrel. 24, Created)
 DT 01-JUN-2003 (TRNMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRNMBLrel. 24, Last annotation update)
 DB L protein (Fragment).
 OS Rabies virus.
 OC ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 OX NCBI_TAXID=11292;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=22541850; PubMed=12655080;
 RX PAEZ A.; NUNEZ C.; GARCIA C.; BOSHELL J.;
 "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192401; AAO31956.1; -.
 FT 28
 SQ SEQUENCE 28 AA; 3010 MW; 2B3637A9AACAA3C6A CRC64;

Query Match Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PRT; 28 AA.
 PRGAP 5
 PRGAP 25

RESULT 58
 Q8OKL5 PRELIMINARY;
 ID Q8OKL5
 AC Q8OKL5;
 DT 01-JUN-2003 (TRNMBLrel. 24, Created)
 DT 01-JUN-2003 (TRNMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TRNMBLrel. 24, Last annotation update)
 DB L protein (Fragment).
 OS Rabies virus.
 OC ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 OX NCBI_TAXID=11292;
 RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=22541850; PubMed=12655080;
 RX PAEZ A.; NUNEZ C.; GARCIA C.; BOSHELL J.;
 "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AF269291; AAF73514.1; -.
 DR PIR; PQ0369; PQ0369.
 FT 28
 SQ SEQUENCE 28 AA; 3024 MW; 2B2237A9AB8F3C6A CRC64;

Query Match Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRT; 28 AA.
 PRGAP 5
 PRGAP 25

RESULT 59
 Q9IWC4 PRELIMINARY;
 ID Q9IWC4
 AC Q9IWC4;
 DT 01-OCT-2000 (TRNMBLrel. 15, Created)
 DT 01-OCT-2000 (TRNMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TRNMBLrel. 15, Last annotation update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 OX NCBI_TAXID=11292;

RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=22541850; PubMed=12655080;
 RX PAEZ A.; NUNEZ C.; GARCIA C.; BOSHELL J.;
 "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AF269292; AAF73514.1; -.
 DR PIR; PQ0369; PQ0369.
 FT 28
 SQ SEQUENCE 28 AA; 3024 MW; 2B24A7A9AACAA3C6A CRC64;

Query Match Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRT; 28 AA.
 PRGAP 5
 PRGAP 25

RESULT 60
 Q9IWC5 PRELIMINARY;
 ID Q9IWC5
 AC Q9IWC5;
 DT 01-OCT-2000 (TRNMBLrel. 15, Created)
 DT 01-OCT-2000 (TRNMBLrel. 15, Last sequence update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC ssRNA negative-strand viruses; Mononegavirales;
 Rhabdoviridae; Lyssavirus.
 OX NCBI_TAXID=11292;

RN [1]_SEQUENCE FROM N.A.
 RP MEDLINE=22541850; PubMed=12655080;
 RX PAEZ A.; NUNEZ C.; GARCIA C.; BOSHELL J.;
 "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AF269291; AAF73514.1; -.
 DR PIR; PQ0369; PQ0369.
 FT 28
 SQ SEQUENCE 28 AA; 3024 MW; 2B24A7A9AACAA3C6A CRC64;

Query Match Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRT; 28 AA.
 PRGAP 5
 PRGAP 25

RESULT 61

DR EMBL; AF189357; AAFL13912.1; -
NON TER 28
SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Gaps 0; PRT; 28 AA.

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 66
Q9QD15 PRELIMINARY; PRT; 28 AA.
ID Q9QD15
AC Q9QD15;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Boschell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AF189353; AF13908.1; -.
NON TER 28
OX NCBI_TaxID=11292;

RP SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Boschell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AF189356; AF13911.1; -.
NON TER 28
SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Gaps 0; PRT; 28 AA.

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 67
Q9QD16 PRELIMINARY; PRT; 28 AA.
ID Q9QD16
AC Q9QD16;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Boschell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AF189353; AF13908.1; -.
NON TER 28
SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Gaps 0; PRT; 28 AA.

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 68
Q9QD17 PRELIMINARY; PRT; 28 AA.
ID Q9QD17
AC Q9QD17;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Boschell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AF189354; AF13908.1; -.
NON TER 28
SEQUENCE 28 AA; 3058 MW; 2E2D37A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Gaps 0; PRT; 28 AA.

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 69
Q9QD18 PRELIMINARY; PRT; 28 AA.
ID Q9QD18
AC Q9QD18;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE L protein (Fragment).
OS Rabies virus.
OC ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; Lyssavirus.
NCBI_TaxID=11292;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Boschell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL; AF189353; AF13908.1; -.
NON TER 28
SEQUENCE 28 AA; 3058 MW; 2E2D37A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; O; Gaps 0; PRT; 28 AA.

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 70
Q9QD19 PRELIMINARY; PRT; 28 AA.
ID Q9QD19
AC Q9QD19;
DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)	RX	MEDLINE=22541850; PubMed=12655080;
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)	RA	Paez A., Nunez C., Garcia C., Boshell J.;
DE	L protein (Fragment).		RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";
OS	Rabies virus.		RL	J. Gen. Virol. 84:795-802(2003).
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;		DR	EMBL; AF189348; AAF13903.1; -.
OC	Rhabdoviridae; Lyssavirus.		FT	NON-TER 28 28
OX	NCBI_TaxID=11292;		SEQUENCE	28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;
RN	SEQUENCE FROM N.A.		QY	1 PRGAP 5
RP	MEDLINE=22541850; PubMed=12655080;		Db	21 PRGAP 25
RX	Paez A., Nunez C., Garcia C., Boshell J.;		RESULT 73	Query Match 25.0%; Score 5; DB 2; Length 28;
RA	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";		Q9QD24	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RT	RT human and dog rabies associated with bats.";		ID	Indels 0; Gaps 0; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RT	J. Gen. Virol. 84:795-802(2003).		AC	PRELIMINARY; PRT; 28 AA.
RL	DR EMBL; AF189352; AAF13907.1; -.		Q9QD24	Query Match 25.0%; Score 5; DB 2; Length 28;
FT	NON-TER 28 28		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
SQ	SEQUENCE 28 AA; 3034 MW; 2E24A7A9AAC3C6A CRC64;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 PRGAP 5		Q9QD24	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Db	21 PRGAP 25		ID	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 74	Query Match 25.0%; Score 5; DB 2; Length 28;		AC	PRELIMINARY; PRT; 28 AA.
Q9QD22	SEQUENCE FROM N.A.		Q9QD24	Query Match 25.0%; Score 5; DB 2; Length 28;
ID	MEDLINE=22541850; PubMed=12655080;		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
AC	Paez A., Nunez C., Garcia C., Boshell J.;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-MAY-2000 (TREMBLrel. 13, Created)		Q9QD24	Query Match 25.0%; Score 5; DB 2; Length 28;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
DE	L protein (Fragment).		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Rabies virus.		Q9QD24	Query Match 25.0%; Score 5; DB 2; Length 28;
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
OC	Rhabdoviridae; Lyssavirus.		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OX	NCBI_TaxID=11292;		Q9QD24	Query Match 25.0%; Score 5; DB 2; Length 28;
RN	SEQUENCE FROM N.A.		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RP	MEDLINE=22541850; PubMed=12655080;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RA	Paez A., Nunez C., Garcia C., Boshell J.;		Q9QD24	Query Match 25.0%; Score 5; DB 2; Length 28;
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RT	J. Gen. Virol. 84:795-802(2003).		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RL	DR EMBL; AF189349; AAF13904.1; -.		Q9QD24	Query Match 25.0%; Score 5; DB 2; Length 28;
FT	NON-TER 28 28		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
SQ	SEQUENCE 28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 PRGAP 5		Q9QD25	Query Match 25.0%; Score 5; DB 2; Length 28;
Db	21 PRGAP 25		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RESULT 75	Query Match 25.0%; Score 5; DB 2; Length 28;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q9QD23	SEQUENCE FROM N.A.		Q9QD25	Query Match 25.0%; Score 5; DB 2; Length 28;
ID	MEDLINE=22541850; PubMed=12655080;		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
AC	Paez A., Nunez C., Garcia C., Boshell J.;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DT	01-MAY-2000 (TREMBLrel. 13, Created)		Q9QD25	Query Match 25.0%; Score 5; DB 2; Length 28;
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
DE	L protein (Fragment).		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OS	Rabies virus.		Q9QD25	Query Match 25.0%; Score 5; DB 2; Length 28;
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
OC	Rhabdoviridae; Lyssavirus.		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OX	NCBI_TaxID=11292;		Q9QD25	Query Match 25.0%; Score 5; DB 2; Length 28;
RN	SEQUENCE FROM N.A.		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RP	MEDLINE=22541850; PubMed=12655080;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RA	Paez A., Nunez C., Garcia C., Boshell J.;		Q9QD25	Query Match 25.0%; Score 5; DB 2; Length 28;
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats.";		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RT	J. Gen. Virol. 84:795-802(2003).		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RL	DR EMBL; AF189346; AAF13901.1; -.		Q9QD25	Query Match 25.0%; Score 5; DB 2; Length 28;
FT	NON-TER 28 28		ID	Best Local Similarity 100.0%; Pred. No. 1.4e+02;
SQ	SEQUENCE 28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;		AC	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 21 PRGAP 25

RESULT 75

Q9QD26 PRELIMINARY; PRT; 28 AA.
 ID Q9QD26; PRELIMINARY; PRT; 28 AA.
 AC Q9QD26; PRELIMINARY; PRT; 28 AA.
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
 DE L protein (Fragment).
 OS Rabies virus.
 OX Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Lyssavirus.
 OX NCBI TaxID:1122;

RN [1] _____

RP SEQUENCE FROM N.A. RP MEDLINE=22541850; PubMed=12655080;
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A., Nunez C., Garcia C., Boshell J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 RT human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AP189345; AAF13900.1; -.
 FT NON-TER 28 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 21 PRGAP 25

Search completed: October 26, 2004, 07:22:24
 Job time : 93.5 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	34	5 ABP33209	ABP33209 Human ova
2	6	30.0	147	2 AY16621	Ay16621 Human ova
3	6	30.0	324	2 AY0348	Ay0348 Murine Ov
4	6	30.0	324	6 ABP97398	ABP97398 Mouse emb
5	6	30.0	358	4 AYG26897	Ayg26897 Novel hum
6	6	30.0	501	4 AAG5822	Aag5822 Human GPR
7	6	30.0	731	7 ADJ71063	Adj71063 Human hea
8	8	30.0	1650	4 ABBS9874	Abbs9874 Drosophil
9	5	25.0	9	2 AAR37732	Aar37732 Collagen-
10	5	25.0	9	2 AAR3239	Aar3239 Collagen-
11	5	25.0	9	2 AAN57686	Aan57686 Collagen-
12	5	25.0	9	5 AAU17113	Aau17113 Human MHC
13	5	25.0	9	5 AAU171607	Aau171607 Human MHC
14	5	25.0	10	5 AAU171662	Aau171662 Human MHC
15	5	25.0	15	2 AAR3209	Aar3209 New contr
16	5	25.0	20	7 ADC9233	Adc9233 Cancer re
17	5	25.0	20	8 ADK01531	Adk01531 Hepatitis
18	5	25.0	25	8 ADM2132	Adm2132 Epib4 blo
19	5	25.0	26	2 AYV20230	Ayv20230 Human bet
20	5	25.0	28	2 AY19651	Ay19651 SEQ ID NO
21	5	25.0	33	3 AAG56952	Aag56952 Arabidops
22	5	25.0	42	5 ADF94734	Adf94734 Hepatitis
23	5	25.0	42	5 ADF94732	Adf94732 Hepatitis
24	5	25.0	44	2 AAW57222	Aaw57222 Targeting
25	5	25.0	46	3 AAY44951	Aay44951 Xenopus t

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	34	5 ABP33209	ABP33209 Human ova
2	6	30.0	147	2 AY16621	Ay16621 Human ova
3	6	30.0	324	2 AY0348	Ay0348 Murine Ov
4	6	30.0	324	6 ABP97398	ABP97398 Mouse emb
5	6	30.0	358	4 AYG26897	Ayg26897 Novel hum
6	6	30.0	501	4 AAG5822	Aag5822 Human GPR
7	6	30.0	731	7 ADJ71063	Adj71063 Human hea
8	8	30.0	1650	4 ABBS9874	Abbs9874 Drosophil
9	5	25.0	9	2 AAR37732	Aar37732 Collagen-
10	5	25.0	9	2 AAR3239	Aar3239 Collagen-
11	5	25.0	9	2 AAN57686	Aan57686 Collagen-
12	5	25.0	9	5 AAU17113	Aau17113 Human MHC
13	5	25.0	9	5 AAU171607	Aau171607 Human MHC
14	5	25.0	10	5 AAU171662	Aau171662 Human MHC
15	5	25.0	15	2 AAR3209	Aar3209 New contr
16	5	25.0	20	7 ADC9233	Adc9233 Cancer re
17	5	25.0	20	8 ADK01531	Adk01531 Hepatitis
18	5	25.0	25	8 ADM2132	Adm2132 Epib4 blo
19	5	25.0	26	2 AYV20230	Ayv20230 Human bet
20	5	25.0	28	2 AY19651	Ay19651 SEQ ID NO
21	5	25.0	33	3 AAG56952	Aag56952 Arabidops
22	5	25.0	42	5 ADF94734	Adf94734 Hepatitis
23	5	25.0	42	5 ADF94732	Adf94732 Hepatitis
24	5	25.0	44	2 AAW57222	Aaw57222 Targeting
25	5	25.0	46	3 AAY44951	Aay44951 Xenopus t

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	34	5 ABP33209	ABP33209 Human ova
2	6	30.0	147	2 AY16621	Ay16621 Human ova
3	6	30.0	324	2 AY0348	Ay0348 Murine Ov
4	6	30.0	324	6 ABP97398	ABP97398 Mouse emb
5	6	30.0	358	4 AYG26897	Ayg26897 Novel hum
6	6	30.0	501	4 AAG5822	Aag5822 Human GPR
7	6	30.0	731	7 ADJ71063	Adj71063 Human hea
8	8	30.0	1650	4 ABBS9874	Abbs9874 Drosophil
9	5	25.0	9	2 AAR37732	Aar37732 Collagen-
10	5	25.0	9	2 AAR3239	Aar3239 Collagen-
11	5	25.0	9	2 AAN57686	Aan57686 Collagen-
12	5	25.0	9	5 AAU17113	Aau17113 Human MHC
13	5	25.0	9	5 AAU171607	Aau171607 Human MHC
14	5	25.0	10	5 AAU171662	Aau171662 Human MHC
15	5	25.0	15	2 AAR3209	Aar3209 New contr
16	5	25.0	20	7 ADC9233	Adc9233 Cancer re
17	5	25.0	20	8 ADK01531	Adk01531 Hepatitis
18	5	25.0	25	8 ADM2132	Adm2132 Epib4 blo
19	5	25.0	26	2 AYV20230	Ayv20230 Human bet
20	5	25.0	28	2 AY19651	Ay19651 SEQ ID NO
21	5	25.0	33	3 AAG56952	Aag56952 Arabidops
22	5	25.0	42	5 ADF94734	Adf94734 Hepatitis
23	5	25.0	42	5 ADF94732	Adf94732 Hepatitis
24	5	25.0	44	2 AAW57222	Aaw57222 Targeting
25	5	25.0	46	3 AAY44951	Aay44951 Xenopus t

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Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	34	5 ABP33209	ABP33209 Human ova
2	6	30.0	147	2 AY16621	Ay16621 Human ova
3	6	30.0	324	2 AY0348	Ay0348 Murine Ov
4	6	30.0	324	6 ABP97398	ABP97398 Mouse emb
5	6	30.0	358	4 AYG26897	Ayg26897 Novel hum
6	6	30.0	501	4 AAG5822	Aag5822 Human GPR
7	6	30.0	731	7 ADJ71063	Adj71063 Human hea
8	8	30.0	1650	4 ABBS9874	Abbs9874 Drosophil
9	5	25.0	9	2 AAR37732	Aar37732 Collagen-
10	5	25.0	9	2 AAR3239	Aar3239 Collagen-
11	5	25.0	9	2 AAN57686	Aan57686 Collagen-
12	5	25.0	9	5 AAU17113	Aau17113 Human MHC
13	5	25.0	9	5 AAU171607	Aau171607 Human MHC
14	5	25.0	10	5 AAU171662	Aau171662 Human MHC
15	5	25.0	15	2 AAR3209	Aar3209 New contr
16	5	25.0	20	7 ADC9233	Adc9233 Cancer re
17	5	25.0	20	8 ADK01531	Adk01531 Hepatitis
18	5	25.0	25	8 ADM2132	Adm2132 Epib4 blo
19	5	25.0	26	2 AYV20230	Ayv20230 Human bet
20	5	25.0	28	2 AY19651	Ay19651 SEQ ID NO
21	5	25.0	33	3 AAG56952	Aag56952 Arabidops
22	5	25.0	42	5 ADF94734	Adf94734 Hepatitis
23	5	25.0	42	5 ADF94732	Adf94732 Hepatitis
24	5	25.0	44	2 AAW57222	Aaw57222 Targeting
25	5	25.0	46	3 AAY44951	Aay44951 Xenopus t

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Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	34	5 ABP33209	ABP33209 Human ova
2	6	30.0	147	2 AY16621	Ay16621 Human ova
3	6	30.0	324	2 AY0348	Ay0348 Murine Ov
4	6	30.0	324	6 ABP97398	ABP97398 Mouse emb
5	6	30.0	358	4 AYG26897	Ayg26897 Novel hum
6	6	30.0	501	4 AAG5822	Aag5822 Human GPR
7	6	30.0	731	7 ADJ71063	Adj71063 Human hea
8	8	30.0	1650	4 ABBS9874	Abbs9874 Drosophil
9	5	25.0	9	2 AAR37732	Aar37732 Collagen-
10	5	25.0	9	2 AAR3239	Aar3239 Collagen-
11	5	25.0	9	2 AAN57686	Aan57686 Collagen-
12	5	25.0	9	5 AAU17113	Aau17113 Human MHC
13	5	25.0	9	5 AAU171607	Aau171607 Human MHC
14	5	25.0	10	5 AAU171662	Aau171662 Human MHC
15	5	25.0	15	2 AAR3209	Aar3209 New contr
16	5	25.0	20	7 ADC9233	Adc9233 Cancer re
17	5	25.0	20	8 ADK01531	Adk01531 Hepatitis
18	5	25.0	25	8 ADM2132	Adm2132 Epib4 blo
19	5	25.0	26	2 AYV20230	Ayv20230 Human bet
20	5	25.0	28	2 AY19651	Ay19651 SEQ ID NO
21	5	25.0	33	3 AAG56952	Aag56952 Arabidops
22	5	25.0	42	5 ADF94734	Adf94734 Hepatitis
23	5	25.0	42	5 ADF94732	Adf94732 Hepatitis
24	5	25.0	44	2 AAW57222	Aaw57222 Targeting
25	5	25.0	46	3 AAY44951	Aay44951 Xenopus t

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Result No.	Score	Query Match	Length	DB ID	Description
1	6	30.0	34	5 ABP33209	ABP33209 Human ova
2	6	30.0	147	2 AY16621	Ay16621 Human ova
3	6	30.0	324	2 AY0348	Ay0348 Murine Ov
4	6	30.0	324	6 ABP97398	ABP97398 Mouse emb
5	6	30.0	358	4 AYG26897	Ayg26897 Novel hum
6	6	30.0	501	4 AAG5822	Aag5822 Human GPR
7	6	30.0	731	7 ADJ71063	Adj71063 Human hea
8	8	30.0	1650	4 ABBS9874	Abbs9874 Drosophil
9	5	25.0	9	2 AAR37732	Aar37732 Collagen-
10	5	25.0	9	2 AAR3239	Aar3239 Collagen-
11	5	25.0	9	2 AAN57686	Aan57686 Collagen-
12	5	25.0	9	5 AAU17113	Aau17113 Human MHC
13	5	25.0	9	5 AAU171607	Aau171607 Human MHC
14	5	25.0	10	5 AAU171662	Aau171662 Human MHC
15	5	25.0	15	2 AAR3209	Aar3209 New contr
16	5	25.0	20	7 ADC9233	Adc9233 Cancer re
17	5	25.0	20	8 ADK01531	Adk01531 Hepatitis
18	5	25.0	25	8 ADM2132	Adm2132 Epib4 blo
19	5	25.0	26	2 AYV20230	Ayv20230 Human bet
20	5	25.0	28	2 AY19651	Ay19651 SEQ ID NO
21	5	25.0	33	3 AAG56952	Aag56952 Arabidops
22	5	25.0	42	5 ADF94734	Adf94734 Hepatitis
23	5	25.0	42	5 ADF94732	Adf94732 Hepatitis
24	5	25.0	44	2 AAW57222	Aaw57222 Targeting
25	5	25.0	46	3 AAY44951	Aay44951 Xenopus t

8

99 5 25.0 86 4 AAM18310 Peptide #
100 5 25.0 86 4 AAM70473 Human bon

ALIGNMENTS

RESULT 1
ID ABP43209 standard; protein; 34 AA.

XX AC ABP43209;

XX DT 22-AUG-2002 (First entry)

XX DE Human ovarian antigen HVDQ49, SEQ ID NO:4341.

XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

KW ovarian cancer; breast cancer; tumour; reproductive system disorder;

KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;

KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;

KW inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder;

KW gastrointestinal disorder; urinary system disorder; drug screening;

KW gene therapy; chromosome mapping; forensic analysis;

KW antibody preparation; cytotoxic; immunomodulatory; neuroprotective;

KW antiinflammatory; gynaecological; reproductive.

XX OS Homo sapiens.

XX PN WO200200677-A1.

XX PD 03-JAN-2002.

XX PP 07-JUN-2001; 2001WO-US018569.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PR Birse CE, Rosen CA;

XX DR WPI: 2002-147878/19.

XX DR N-PSDB: ABQ56286.

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

XX PS Claim 11; SEQ ID NO 4341; 2922pp; English.

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ4131-ABQ5305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosis or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may

further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 34 AA;

Query Match	Score	DB
Best Local Similarity	6	5;
Matches	6;	Pred. No. 15;
Conservative	0;	Mismatches
	0;	Indels
	0;	Gaps

XX Qy 15 LETMFL 20

XX Db 2 LETMFL 7

RESULT 2

XX AAY76621 standard; protein; 147 AA.

XX ID AAY76621

XX XX Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment.

XX DT 10-APR-2000 (first entry)

XX DE Human ovarian tumor EST fragment encoded protein 117.

XX KW Human ovarian tumor EST fragment encoded protein 117.

XX XX Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment.

XX XX DE Human ovarian tumor EST fragment encoded protein 117.

XX KW Human ovarian tumor EST fragment encoded protein 117.

XX XX DB19817557-Al.

XX XX PR 09-APR-1998;

XX XX DR 09-APR-1998;

XX XX DR 09-APR-1998;

XX XX PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX XX PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX XX WPI: 1999-591920/51.

XX XX DR N-PSDB; AA277497.

XX XX PT New nucleic acid sequences expressed in ovarian, and some other, cancer tissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents.

XX PT PI Claim 25; Page 292; 310pp; German.

XX PS This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies.

CC (A) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so

CC CC should reduce the number of failures associated with the fact that ESTS

CC CC from different libraries may represent different parts of the same

CC CC unknown gene, distorting the estimated frequency of occurrence in a

CC CC particular tissue. AA76505-Y7638 represent protein fragments encoded by

CC CC the human ovarian tumor cDNA library derived EST fragments represented in

CC AA77450-Z77572

AC	ABC26897;	DT	30-JAN-2002	(first entry)
XX	18-FEB-2002	(first entry)	XX	XX
DT	Novel human diagnostic protein #26888.	DE	Human GPR38 variant GPR38V polypeptide.	XX
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.	XX	GPR38V; variant; antibacterial; cytostatic; analgesic; antiasthmatic; ant-Parkinsonian; hypotensive; antidiabetic; osteopathic; ant-allergic; antimigraine; neuroleptic; nootropic; anticonvulsant; antulcer; antiemetic; cardiant; vaccine; human.	XX
XX	Homo sapiens.	OS	Home sapiens.	XX
XX	WO2001175067-A2.	PN	WO200164936-A2.	XX
XX	PD	PD	07-SEP-2001.	XX
XX	11-OCT-2001.	XX	28-FEB-2001; 2001WO-US006277.	XX
XX	30-MAR-2001; 2001WO-US008631.	PR	01-MAR-2000; 2000US-00516315.	XX
XX	31-MAR-2000; 2000US-00540217.	PA	(SMIK) SMITHKLINE BEECHAM CORP.	XX
XX	23-AUG-2000; 2000US-00649167.	PA	Elshourbagy N, Shabon U;	XX
XX	(NYSE-) HYSEQ INC.	P1	WPI; 2001-638956/73.	XX
XX	PA	DR	DR N-PSDB; AAI66989.	XX
XX	DR	DR	New human GPR38V polypeptide and Polynucleotide, useful for treating e.g. bacterial, fungal, protozoal and viral infections, cancers or allergies, as vaccines, and for identifying agonists and antagonists potentially useful in therapy.	PT
XX	WPI; 2001-639362/73.	PS	Claim 1: Page 26; 32pp; English.	XX
XX	N-PSDB; AAS91084.	XX	This represents a human GPR38 variant (GPR38V) polypeptide. GPR38V can be expressed by standard recombinant methodology. The polynucleotides and polypeptides are used in the treatment of bacterial, fungal, protozoal and viral infections, caused by HIV-1 or HIV-2, pain, cancers, diabetes, obesity, anorexia, asthma, Parkinson's disease, acute heart failure, hypertension, urinary retentions, osteoporosis, allergies, ulcers, migraine, psychotic and neurological disorders, or dyskinesias. They are also useful for identifying agonists and antagonists that are potentially useful in therapy, as vaccines to induce immunological response in a mammal. The polypeptides may also be used as immunogens to produce antibodies immunospecific for the polypeptides, and to identify membrane bound or soluble receptors	PT
XX	PS	XX	Sequence 501 AA;	SQ
XX	PS	XX	Query Match 30.0%; Score 6; DB 4; Length 501; Best Local Similarity 100.0%; Pred. No. 1.4e-02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0	XX
XX	PS	XX	Qy 1 PRGAPM 6 Db 85 PRGAPM 90	XX
XX	PS	XX	RESULT 7 ADJ71063	DE
XX	PS	XX	Query Match 30.0%; Score 6; DB 4; Length 358; Best Local Similarity 100.0%; Pred. No. 1e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0	ID
XX	PS	XX	Qy 15 LETMFL 20 Db 39 LETMFL 44	ID ADJ71063 standard; protein; 731 AA.
XX	PS	XX	RESULT 6 AAG65822	KW Huntington's disease; osteoarthritis;
XX	PS	XX	Qy 15 LETMFL 20 Db 39 LETMFL 44	KW Leber's hereditary optic neuropathy; LHON;
XX	PS	XX	Qy 15 LETMFL 20 Db 39 LETMFL 44	KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX	PS	XX	Qy 15 LETMFL 20 Db 39 LETMFL 44	KW myoclonic epilepsy, ragged red fiber syndrome; MERRF; cancer;
XX	PS	XX	Qy 15 LETMFL 20 Db 39 LETMFL 44	KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
XX	PS	XX	Qy 15 LETMFL 20 Db 39 LETMFL 44	KW Human heat mitochondrial protein as a therapeutic target SeqID2869.

KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX WO2003087768-A2.
XX 23-OCT-2003.
PD XX 04-APR-2003; 2003WO-US010870.
PF XX 12-APR-2002; 2002US-0372843P.
PR PR 17-JUN-2002; 2002US-038987P.
PR PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX PT Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX DR WI; 2003-845369/78.
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX PS SEQ ID NO 2869; 180pp; English.
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX SQ Sequence 731 AA;
Query Match 30.0%; Score 6; DB 7; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAPM 6
Db 542 PRGAPM 547
RESULT 8
ABB5984 ID ABB59874 standard; protein; 1630 AA.
XX AC ABB59874;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 6414.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009331.
XX PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-0061450.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX DR WPI; 2001-656860/75.
DR N-PSDB; ABL03977.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
interactions.
XX Disclosure; SEQ ID NO 6414; 21pp + Sequence Listing; English.
XX PS
XX CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL0511), expressed DNA
CC sequences (ABL0840-ABL1675) and the encoded proteins (ABL16176-
CC ABB7202). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 1630 AA;
Query Match 30.0%; Score 6; DB 4; Length 1630;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 QMLETM 18
Db 1254 QMLETM 1259
RESULT 9
AAR37732 ID AAR37732 standard; peptide; 9 AA.
XX AC AAR37732;
XX DT 25-MAR-2003 (revised)
DT 07-SEP-1993 (first entry)
XX DE Collagen-like polymer #15
KW Synthetic.
XX PN WO9310154-A1.
XX PD 27-MAY-1993.
XX PP 04-NOV-1992; 92WO-US009485.
XX PR 12-NOV-1991; 91US-00791960.
DA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX PI Cappello J, Ferrari FA;
DR WPI; 1993-182495/22.

PT High mol. wt. collagen-like protein polymers - capable of being produced
 PT in unicellular microorganisms.
 XX Disclosure; Page 12; 82pp; English.
 XX
 CC The sequences given in AAR37718-32 are examples of recombinantly produced
 CC collagen-like polymers (CLPs) which consist of repeated tripeptide
 CC sequences selected from a wide range of GXy sequences, where X and Y can
 CC be any amino acid. These polymers have molecular weights of >30 kD and
 CC are able to form helices due to interchain linkages. These polymers pref.
 CC contain a proportion of tripeptide triad sequences found in natural
 CC collagens, pre/pro-mammalian collagens. The CLPs impart unique
 CC characteristics to materials such as fibres, membranes, films, coatings,
 CC hydrogels, colloid suspensions and moulded articles. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 9 AA;

Query Match 25.0%; Score 5; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 | | | |
 Db 5 PRGAP 9

RESULT 10

AAR93239
 ID AAR93239 standard; peptide, 9 AA.
 XX
 AC AAR93239;

XX DT 25-MAR-2003 (revised)
 DT 24-FEB-1996 (first entry)

XX DE Collagen-like GUB sequence motif 5.
 XX KW collagen; repetitive triad motif; recombinant production; photographic;
 KW medical; structural; fibre.
 OS Synthetic.
 XX PN US5496712-A.
 XX PD 05-MAR-1996.
 XX PP 05-NOV-1992; 92US-00972032.

XX PR 06-NOV-1990; 90US-00609716.
 PR 12-NOV-1991; 91US-00791560.
 XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 XX PI Cappello J, Ferrari FA;
 XX DR WPI; 1996-150728/15.

XX Collagen-like polymers comprising repetitive triads - produced in
 PT unicellular organisms with improved characteristics, useful in, e.g.
 PT photographic and medical fibres.
 XX Disclosure; Col 6; 43pp; English.
 XX
 PT The invention concerns collagen-like polymers having repetitive triads
 CC with reduced proline content, and where glycine is the initial amino acid
 CC and the subsequent amino acids are varied. The choice of triads utilised
 CC in a recombinant collagen-like polymer are chosen in order to affect
 CC properties such as helix stability, hydration, solubility, gel point,
 CC biodegradation and immunogenicity. Also considered is the level of
 CC guanidine and cytosine nucleotides (due to levels of glycine and proline)
 CC present in the genes encoding the polymers. As the gene is synthesised
 CC there is opportunity for strands to loop out, single-stranded DNA to be

CC excised, recombination events to occur which can result in loss of
 CC segments of the gene, and inefficient transcription and/or translation
 CC (due to the presence of self-complementary sequences), hence genes of the
 CC invention are designed to provide the advantageous properties of high
 CC collagen, while at the same time allowing for stable expression of high
 CC mol. wt. collagen-like proteins. Triads of particular interest include
 CC GAP, GPA, CPP, GAS, GPC, GPS, GAO, GSP, GAK, GPR, GPK, GAI, GER,
 CC GDR, GBP, GDA, GAH and GIA. The collagen-like polymers may impart new
 CC characteristics, finding wide use in photographic, medical, structural
 CC and fibre applications, and are capable of being produced in unicellular
 CC microorganisms at high mol. wts. and in high efficiency. AAR93235-39 are
 CC peptides defining GUB (sic) sequences. The peptides are useful as
 CC haptogens, to produce antisera or monoclonal antibodies specific to the
 CC sequences which are then used for affinity purification, identification
 CC of the polymers, etc. (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 9 AA;

Query Match 25.0%; Score 5; DB 2; Length 9;
 Best Local Similarity 100.0%; pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 | | | |
 Db 5 PRGAP 9

RESULT 11

AAW57686
 ID AAW57686 standard; peptide, 9 AA.
 XX
 AC AAW57686;

XX DT 27-AUG-1998 (first entry)
 XX DE Collagen-like polymer fragment.

XX KW Collagen-like polymer; synthetic polymer; fibre coating;
 KW prosthetic device; catalytic substance.
 OS Synthetic.
 XX PN US5773249-A.
 XX PD 30-JUN-1998.
 XX PP 02-MAY-1996; 96US-00642255.

XX PR 04-NOV-1986; 86US-00927258.
 PR 29-OCT-1987; 87US-00114618.
 PR 09-NOV-1988; 88US-00269439.
 PR 06-NOV-1990; 90US-00609716.
 PR 12-NOV-1991; 91US-00791560.
 PR 05-NOV-1992; 92US-0072032.
 PR 22-DEC-1995; 95US-00577046.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 XX PI Ferrari FA, Cappello J;
 XX DR WPI; 1998-387004/33.

XX Recombinant collagen-like polymers - useful for making gels, films,
 PT fibres, etc.
 XX Disclosure; Col 6; 93pp; English.
 XX
 CC This sequence represents a fragment of an unnatural collagen-like polymer
 CC objects and admixed with other natural or synthetic polymers or coatings
 CC on fibres, films, labware or other surfaces, e.g. prosthetic devices. The
 CC polymers may be used for binding a wide variety of specific binding

Qy	1 PRGAP 5 	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 15 AAR93209 standard; peptide; 15 AA.
Db	2 PRGAP 6		ID AAR93209; XX AC AAR93209; XX DT 04-OCT-1996 (first entry)
RESULT 14			
AAU71662	ID AAU71662 standard; peptide; 10 AA.		XX New contraceptive peptide #5 derived from Zona Pellucida ZP3 protein.
XX			XX Zona pellucida; ZP3; vaccine; humoral response; contraception; epitope;
AC			KW pathogenic T cell response; ovary; assay; autoimmune; antibody;
AAU71662;			KW passive immunisation.
XX			XX Synthetic.
DT 26-FEB-2002	(First entry)		OS
XX			XX DE Human MHC class I molecule HLA-B7 binding 103P3E8 peptide #69.
DE			XX WO9606113-A1.
XX			XX KW prostate; bladder; kidney; colon; lung; breast; rectum; stomach;
KW			KW tumour; cancer; cytostatic; gene therapy; antibody therapy; ribozyme;
KW			KW single chain monoclonal antibody; serum; blood; urine; tissue; human;
KW			KW chromosome 9q13-q21.
XX			XX OS Homo sapiens.
OS			XX PN WO200179557-A2.
XX			XX PD 25-OCT-2001.
PD			XX XX DR 12-APR-2001; 2001WO-US012181.
XX			XX XX PR 12-APR-2000; 2000US-0196647P.
PR			XX XX PA (ALKU) AKZO NOBEL NV.
XX			XX XX PI van Duin M, Grootenhuis AJ, Bunschoten EJ;
PA			XX XX DR WPI; 1996-151331/15.
(UROG-)			XX XX PS Claim 5; Page 31; 43PP; English.
UROGENESIS INC.			XX XX PS Claim 5; Page 31; 43PP; English.
XX			CC Peptides AAR93205-9 are examples of peptides derived from the sequence of
PI			CC the Zona Pellucida protein ZP3 which contain the amino acid sequences
Jakobovits A;			CC AAR93210 or AAR93214-5. The peptides are esp. based on amino acids 23-30
XX			CC of the ZP3 protein. The novel peptides can be used in vaccines to induce
DR 2002-061976/08.			CC a humoral response against the ZP3 protein e.g. for contraception, esp.
XX			CC as they do not raise a pathogenic T cell response since they do not
PR Monitoring 103P3E8 gene products in sample from patient (suspected of			CC contain T cell epitopes. The novel peptides thus avoid potential ovarian
PR having cancer, useful for diagnosing, managing or treating cancers, e.g.			CC damage caused by some peptides used as vaccines. The peptides are also
PR prostate cancer, comprises determining presence of aberrant 103P3E8 gene			CC useful in assays for detecting autoimmune antibodies or for generating
XX products.			CC antibodies for passive immunisation
PS Disclosure; Page 96; 128PP; English.			XX XX SQ Sequence 15 AA;
XX Sequences AAU71093-AAU71796 represent the 103P3E8-related protein and			Query Match Score 5; DB 2; Length 15;
CC peptide fragments of the protein. 103P3E8 exhibits tissue specific			Best Local Similarity 25.0%; Pred. No. 1e+02 , Mismatches 0; Indels 0; Gaps 0;
CC expression in normal adult tissue, but it is also aberrantly expressed in			CC Matches 5; Conservative 0;
CC many cancers including tumours of the prostate, bladder, kidney, colon,			CC
CC lung, breast, rectum and stomach. The 103P3E8 polynucleotide, its related			CC
CC protein and peptide fragments and specific PCR primers are therefore			CC
CC useful for diagnosing and treating cancer. A vector comprising a			CC
CC polynucleotide which encodes a single chain monoclonal antibody, that			CC
CC immunospecifically binds to an 103P3E8-related protein, and a ribozyme			CC
CC capable of cleaving a polynucleotide having the 103P3E8 coding sequence,			CC
CC are both useful in the preparation of a composition for treating a			CC
CC patient with a cancer that expresses 103P3E8. The sequences can be used			CC
CC in diagnostic methods to monitor the level of 103P3E8 gene products in			CC
CC serum, blood, urine and tissue and to thereby detect the presence of			CC
CC cancerous cells			CC XX SQ Sequence 10 AA;
XX			Query Match Score 5; DB 5; Length 10;
CC Best Local Similarity 100.0%; Pred. No. 73, Mismatches 0; Indels 0; Gaps 0;			Best Local Similarity 25.0%; Pred. No. 1e+02 , Mismatches 0; Indels 0; Gaps 0;
CC Matches 5; Conservative 0;			CC Matches 5; Conservative 0;
DB 2 PRGAP 5			CC
DB 2 PRGAP 6			CC XX DT 01-JAN-2004 (first entry)
QY			XX DE Cancer-related DGI-2-binder peptide - SEQ ID 66.
XX			XX XX KW cytosstatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; HRas;
KW			KW IGF-1; VEGF; vascular endothelial growth factor receptor; VEGFR-1;
VEGF-R2; VEGF-R3; FGF1; FMS-related tyrosine kinase 1; FAK1; KDR;			KW kinase insert domain protein receptor; EGFR; epidermal growth factor;
FGR1; fibroblast growth factor; Tie-1.			KW

XX	DR	WPI; 2004-169243/16.
IS	XX	Unidentified.
IN	XX	WO2003035839-A2.
XX	XX	01-MAY-2003.
XX	XX	24-OCT-2002; 2002WO-US034021.
XX	XX	24-OCT-2001; 2001US-0345471P.
XX	XX	(DGIB-) DGI BIOTECHNOLOGIES INC.
XX	XX	Pillula RC, Brissette R, Spruyt M, Dedova O, Blume A;
XX	XX	Prendergast J, Goldstein N;
XX	XX	WPI; 2003-457332/43.
XX	XX	Selecting target and target binder pairs for preparing a composition for treating cancer by mixing in a reaction vessel phage expressing target binders and phage expressing target binders.
XX	XX	Claim 26; SEQ ID NO 66; 172pp; English.
XX	XX	The invention relates to a novel method of selecting target and target binder pairs comprising mixing in a reaction vessel phage expressing biological targets and phage expressing target binders, each having distinguishable selection markers and selecting target and target binder pairs based on the selection markers. The molecules of the invention demonstrate cytostatic activity whilst the method may be useful for selecting target and target binder pairs for preparing a composition for treating cancer. Furthermore, the method may be utilised during gene therapy procedures. The current sequence is that of the cancer-related DGI-2 binder peptide of the invention.
XX	XX	Sequence 20 AA;
XX	XX	Query Match Score 5; DB 8; Length 20;
XX	XX	Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX	XX	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	XX	QY 1 PRGAP 5
XX	XX	DB 7 PRGAP 11
XX	XX	RESULT 18
XX	XX	ID ADM32132 standard; protein; 25 AA.
XX	XX	AC ADM32132;
XX	XX	AC 17-JUN-2004 (first entry)
XX	XX	DT DT
XX	XX	DE EphB4 blocking peptide 6, seq id 7.
XX	XX	KW Cytostatic; gene therapy; Inhibitor; cancerous growth; cancer; breast; prostate; ephrin type-B receptor 4 precursor; EphB4; human.
XX	XX	OS Homo sapiens.
XX	XX	PN WO200424773-A1.
XX	XX	PD 25-MAR-2004.
XX	XX	PF 16-SEP-2003; 2003WO-AU001209.
XX	XX	PR 16-SEP-2002; 2002AU-00951409.
XX	XX	PA (QUBE-) QUEEN ELIZABETH HOSPITAL.
XX	XX	PI Stephenson S;
XX	XX	DR WPI; 2004-270012/25.
XX	XX	Inhibiting cancerous growth of a cell by contacting the cell with an antibody, or its antigen-binding portion, that binds to an epitope of EphB4 polypeptide.
XX	XX	Example 6; SEQ ID NO 7; 73pp; English.
XX	XX	The invention relates to a method of inhibiting cancerous growth of a cell, comprising contacting the cell with at least one antibody, or its antigen-binding portion, where the antibody or antigen-binding portion binds to an epitope located within residues 200-400 of EphB4, which consists of the sequence of 984 amino acids (S1) fully defined in the specification, or to an epitope located in a sequence at least 85% identical to residues 200-400 of EphB4 or 220-230 of EphB4. The composition and methods are usefull for treating or preventing cancer.
XX	XX	WPI; 2004-169243/16.
XX	XX	24-JUL-2003; 2003WO-FP008112.
XX	XX	24-JUL-2002; 2002AT-00001124.
XX	XX	11-JUL-2003; 2003EP-00450171.
XX	XX	(INTE-) INTERCELL AG.
XX	XX	Mattner F, Schmidt W, Haberl A;

(e.g. breast or prostate cancer) or for identifying agents that inhibit cancerous growth of a cell. The current sequence represents an EphB4 blocking peptide used in an example from the invention in EphB4 epitope mapping.

XX Sequence 25 AA;

Query Match 25.0%; Score 5; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 15 PRGAP 19

RESULT 19
AYA2030
.ID AYA2030 standard; protein: 26 AA.

XX AAY2030;

XX DT 22-JUL-1999 (first entry)

DE Human beta-amyloid precursor protein mutant fragment 55.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;

KW frameshift mutation; age-related disease; neurodegenerative disorder;

KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;

KW Huntington's disease; multiple sclerosis; alcoholic liver disease;

KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;

KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofibrilament-M;

KW neurofibrilament-F; presenilin I; presenilin II; cellular tumour antigen;

KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUFP-1;

KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;

KW high mobility group protein-C; neuroendocrine specific protein A.

OS Synthetic.

OS Homo sapiens.

XX WO9845322-A2.

XX PN

XX PD 15-OCT-1998.

XX PF 02-APR-1998; 98WO-1B000705.

XX PR 10-APR-1997; 97US-0043163P.

XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYUT-) RIJKSUNIV UTRICHT.

XX PI Van Leeuwen FW,

Grosveld FG,

Burbach JPH;

XX DR 1998-6109901/51.

XX DR N-PSDB; AAX75753.

XX Diagnosing disease by detecting framshift mutations in RNA or

PR corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.

XX Disclosure; Fig 2; 25bp; English.

CC This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be

CC caused by mutations in RNA rather than DNA. The invention describes the use of neuronal system RNA molecules, specifically proteins associated with the microtubule-associated protein (beta-APP), the microtubule-associated protein Tau and Big Tau, ubiquitin B, apolipoprotein E, neurofilament-L, neurofibril filament-M, neurofibril filament-F, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUFP-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A.

CC protein-C (HMGP-C) and neuroendocrine specific protein A.

XX Sequence 26 AA;

Qy 1 PRGAP 5
Db 5 PRGAP 9

RESULT 20
AYA19651
.ID AYA19651 standard; protein: 28 AA.

XX AAY19651;

XX DT 14-JUL-1999 (first entry)

XX SEQ ID NO 369 from WO9922243.

XX Human secreted protein; cancer; tumour; neurodegenerative disorder; developmental abnormality; fetal deficiency; blood disorder; leukemia; immune system disease; autoimmune disease; hepatic disease; renal disease; lymphoma; inflammation; allergy; ischemic shock; Alzheimer's; cognitive disorder; schizophrenia; prostate disease; obesity; osteoporosis; arthritis; malignancy; testes disease; lung disease; thymus disease; digestive disorder; endocrine disorder; infection; AIDS.

XX OS Homo sapiens.

XX XX PN WO9922243-A1.

XX PD 06-MAY-1999.

XX PR 23-OCT-1998; 98WO-US022376.

XX PR 24-OCT-1997; 97US-0062784P.

PR 24-OCT-1997; 97US-0063088P.

PR 24-OCT-1997; 97US-0063089P.

PR 24-OCT-1997; 97US-0063090P.

PR 24-OCT-1997; 97US-0063091P.

PR 24-OCT-1997; 97US-0063092P.

PR 24-OCT-1997; 97US-0063093P.

PR 24-OCT-1997; 97US-0063094P.

PR 24-OCT-1997; 97US-0063095P.

PR 24-OCT-1997; 97US-0063096P.

PR 24-OCT-1997; 97US-0063097P.

PR 24-OCT-1997; 97US-0063098P.

PR 24-OCT-1997; 97US-0063099P.

PR 24-OCT-1997; 97US-0063100P.

PR 24-OCT-1997; 97US-0063101P.

PR 24-OCT-1997; 97US-0063109P.

PR 24-OCT-1997; 97US-0063110P.

PR 24-OCT-1997; 97US-0063111P.

PR 24-OCT-1997; 97US-0063148P.

PR 24-OCT-1997; 97US-0063388P.

XX (HUMA-) HUMAN GENOME SCI INC.

CC Feng P, Rosen CA, Ruben SM, Ni J, Wei Y, Soppet DR, Moore PA;

CC Shi Y, Bigner DW, Olsen HS, Bigner RR, Young P;

CC PI Greene JM, Lafleur KA, Florence C, Duan DR, Janat F, Endress GA;

CC Carter KC;

WPI; 1999-303069/25.
 DR New isolated human genes and the secreted polypeptides they encode.
 XX Disclosure; Page 485; 546pp; English.
 XX The specification describes human secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the polypeptides in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and fetal deficiencies, blood disorders, leukaemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, ischaemic shock, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, obesity, disorders involving osteoclasts such as osteoporosis, arthritis or malignancies, diseases of testes, lung or thymus, digestive endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners.

XX Sequence 28 AA;
 SQ 25.0%; Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 COMLE 16
 Db 3 COMLE 7

RESULT 21
 AAG56932
 ID AAG56952 standard; protein; 33 AA.
 XX DT 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 73318.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; Genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX EP1033405-A2.
 FN 06-SEP-2000.
 PD 25-FEB-2000; 2000EP-00301439.
 XX PR 25-FEB-1999; 99US-0121845P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-013548P.
 PR 23-MAR-1999; 99US-0125738P.
 PR 25-MAR-1999; 99US-0126264P.
 PR 29-MAR-1999; 99US-0126784P.
 PR 01-APR-1999; 99US-0127462P.
 PR 06-APR-1999; 99US-0128234P.
 PR 08-APR-1999; 99US-0128714P.
 PR 16-APR-1999; 99US-0129845P.
 PR 19-APR-1999; 99US-0130077P.
 PR 21-APR-1999; 99US-013049P.
 PR 23-APR-1999; 99US-0130510P.
 PR 23-APR-1999; 99US-0130891P.
 PR 28-APR-1999; 99US-013149P.
 PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.
 PR 04-MAY-1999; 99US-0132404P.
 PR 05-MAY-1999; 99US-0132405P.
 PR 06-MAY-1999; 99US-0132406P.
 PR 07-MAY-1999; 99US-0132407P.
 PR 11-MAY-1999; 99US-0132408P.
 PR 14-MAY-1999; 99US-0134218P.
 PR 14-MAY-1999; 99US-0134219P.
 PR 14-MAY-1999; 99US-0134211P.
 PR 18-MAY-1999; 99US-0134310P.
 PR 19-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134911P.
 PR 21-MAY-1999; 99US-0135144P.
 PR 21-MAY-1999; 99US-0135333P.
 PR 24-MAY-1999; 99US-0135659P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0137222P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137529P.
 PR 07-JUN-1999; 99US-0137744P.
 PR 08-JUN-1999; 99US-0138049P.
 PR 10-JUN-1999; 99US-0138409P.
 PR 14-JUN-1999; 99US-0138817P.
 PR 16-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139422P.
 PR 16-JUN-1999; 99US-0139433P.
 PR 17-JUN-1999; 99US-0139432P.
 PR 18-JUN-1999; 99US-0139434P.
 PR 18-JUN-1999; 99US-0139435P.
 PR 18-JUN-1999; 99US-0139436P.
 PR 18-JUN-1999; 99US-0139437P.
 PR 18-JUN-1999; 99US-0139438P.
 PR 18-JUN-1999; 99US-0139439P.
 PR 18-JUN-1999; 99US-0139440P.
 PR 18-JUN-1999; 99US-0139441P.
 PR 18-JUN-1999; 99US-0139446P.
 PR 18-JUN-1999; 99US-0139447P.
 PR 18-JUN-1999; 99US-0139448P.
 PR 18-JUN-1999; 99US-0139449P.
 PR 18-JUN-1999; 99US-0139450P.
 PR 18-JUN-1999; 99US-0139451P.
 PR 18-JUN-1999; 99US-0139452P.
 PR 18-JUN-1999; 99US-0139453P.
 PR 18-JUN-1999; 99US-0139730P.
 PR 18-JUN-1999; 99US-0139733P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 18-JUN-1999; 99US-0139818P.
 PR 18-JUN-1999; 99US-0139819P.
 PR 23-JUN-1999; 99US-0140333P.
 PR 23-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0139733P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140921P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUN-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-014205P.
 PR 06-JUL-1999; 99US-014230P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0140921P.
 PR 12-JUL-1999; 99US-0142940P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-014364P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 19-JUL-1999; 99US-014434P.
 PR 19-JUL-1999; 99US-014435P.
 PR 20-JUL-1999; 99US-0144452P.
 PR 20-JUL-1999; 99US-0144453P.
 PR 21-JUL-1999; 99US-0144614P.
 PR 21-JUL-1999; 99US-0145086P.

PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160808P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160811P.
PR	23-JUL-1999;	99US-0145244P.	PR	22-OCT-1999;	99US-0160898P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-014551P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146316P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161929P.
PR	04-AUG-1999;	99US-0147204P.	PR	28-OCT-1999;	99US-0161933P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147204P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	09-AUG-1999;	99US-0147433P.			
PR	09-AUG-1999;	99US-0147915P.			
PR	10-AUG-1999;	99US-0147917P.			
PR	11-AUG-1999;	99US-0148319P.			
PR	12-AUG-1999;	99US-0148341P.			
PR	13-AUG-1999;	99US-0148555P.			
PR	13-AUG-1999;	99US-0148684P.			
PR	16-AUG-1999;	99US-0149368P.			
PR	17-AUG-1999;	99US-0149375P.			
PR	18-AUG-1999;	99US-0149416P.			
PR	20-AUG-1999;	99US-0149722P.			
PR	20-AUG-1999;	99US-0149733P.			
PR	20-AUG-1999;	99US-0149939P.			
PR	23-AUG-1999;	99US-0149902P.			
PR	23-AUG-1999;	99US-0149930P.			
PR	25-AUG-1999;	99US-0150566P.			
PR	26-AUG-1999;	99US-0150844P.			
PR	27-AUG-1999;	99US-0151065P.			
PR	27-AUG-1999;	99US-0151066P.			
PR	30-AUG-1999;	99US-0151080P.			
PR	31-AUG-1999;	99US-0151130P.			
PR	01-SEP-1999;	99US-0151438P.			
PR	07-SEP-1999;	99US-0151930P.			
PR	10-SEP-1999;	99US-0152363P.			
PR	13-SEP-1999;	99US-0153070P.			
PR	15-SEP-1999;	99US-0153738P.			
PR	16-SEP-1999;	99US-0154018P.			
PR	16-SEP-1999;	99US-0154039P.			
PR	20-SEP-1999;	99US-0154779P.			
PR	22-SEP-1999;	99US-0155199P.			
PR	23-SEP-1999;	99US-0154848P.			
PR	24-SEP-1999;	99US-0155655P.			
PR	28-SEP-1999;	99US-0155648P.			
PR	29-SEP-1999;	99US-0155868P.			
PR	12-OCT-1999;	99US-0158369P.			
PR	13-OCT-1999;	99US-0157733P.			
PR	13-OCT-1999;	99US-0158294P.			
PR	13-OCT-1999;	99US-0159295P.			
PR	14-OCT-1999;	99US-0159322P.			
PR	14-OCT-1999;	99US-0159333P.			
PR	14-OCT-1999;	99US-0159331P.			
PR	14-OCT-1999;	99US-0159631P.			
PR	14-OCT-1999;	99US-0159638P.			
PR	18-OCT-1999;	99US-0159584P.			
PR	21-OCT-1999;	99US-0160744P.			

Query Match 25.0%; Score 5; DB 3+; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.9e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QMLET 17
Db 26 QMLET 30

RESULT 22
ADF94734
ID ADF94734 standard; protein; 42 AA.
XX ADF94734;
AC ADF94734;
DT 26-FEB-2004 (first entry)
XX Hepatitis D virus type III antigen protein fragment, SEQ ID 9.
DE Hepatitis D virus type III antigen; RNA polymerase II.
XX Virucide; hepatitis D virus antigen; HDV antigen; RNA polymerase II.
XX Hepatitis D virus.
XX WO200268655-A1.
XX PD 06-SEP-2002.
XX DT 27-FEB-2002; 2002WO-JP001817.
XX PR 27-FEB-2001; 2001JP-00053163.
PA (CIRC-) CIRCLE PROMOTION SCI & ENG.
PA (KYOW) KYOWA HAKKO KOGYO KK.
PI Handa H, Yamaguchi Y;
XX DR WPI; 2002-698673/75.
XX Non-infective cell-requiring method of searching for hepatitis D remedies
PT in a system containing e.g. polypeptide binding to RNA polymerase II with
PT measuring of binding level for indication.
XX Claim 5; SEQ ID NO 9; 84pp; Japanese.
XX The present invention relates to a method for searching hepatitis D
CC remedies. The method comprises adding a test compound to a system
CC containing e.g. a hepatitis D virus antigen (HDV antigen) and RNA
CC polymerase II, measuring the binding level of HDV antigen binding to RNA
CC polymerase II, and comparing with a control for selection of a compound
CC inhibiting the binding. The method is for screening remedies for
CC hepatitis D including for hepatitis virus D accompanying hepatitis B,
CC such as gene expression promoters applicable in regeneration medicine for
CC treating organs or tissues. The present sequence is a HDV antigen
CC sequence.

XX	SQ Sequence 42 AA;	AC AAW57222;	XX	04-AUG-1998 (first entry)
Query Match	25.0%; Score 5; DB 5; Length 42;	DT 04-AUG-1998 (first entry)	XX	
Best Local Similarity	100.0%; Pred. No. 2.4e+02;	DE Targeting vector Tg-2/Not containing PGK-neomycin-resistant gene protein.	XX	
Matches	5; Conservative 0; Mismatches 0;	XX		
Qy	1 PRGAP 5	KW Targeting vector; Tg-2/Not; nucleobindin; screening; nephritis;	XX	
Db	14 PRGAP 18	KW blood vessel; inflammation; PGK-neomycin-resistant gene.	XX	
		XX Synthetic.	OS	
		XX JP10117633-A.	PN	
		XX PD 12-MAY-1998.	XX	
		XX PF 21-OCT-1996; 96JP-00298219.	XX	
		XX PR 21-OCT-1996; 96JP-00298219.	XX	
		XX PA (MITSU-) MITSUI SEIYAKU KOGYO KK.	PA	
		PA (KANA/) KANRI Y. PA (FUJI-) FUJITA GAKUEN.	PA	
		XX DR WPI: 1998-325762/29.	XX	
		DR N-PSDB; AAV28851.	DR	
		XX PT Gene-deleted animal e.g. mouse - useful for screening therapeutic agents for diseases such as blood vessel inflammation and nephritis.	PT	
		XX PS Example 2: Fig 3; 11pp; Japanese.	PS	
		XX XX The present sequence represents a protein from a targeting vector Tg-2/Not containing a PGK-neomycin-resistant gene, from the present invention. The targeting vector is used in an example of the present invention for producing a gene-deleted animal e.g. a mouse comprising no gene to encode nucleobindin in which all or part of nucleobindin gene is deleted or replaced by another gene. The mouse can be used for screening therapeutic agents against diseases such as blood vessel inflammation and nephritis.	CC	
		XX XX PT Sequence 44 AA;	PT	
		XX SQ Query Match 25.0%; Score 5; DB 2; Length 44; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SQ	
		XX PR 27-FEB-2001; 2001JP-00053163.	PR	
		XX (CIRC-) CIRCLE PROMOTION SCI & ENG.	(CIRC-)	
		PA (KIYOWA) KIYOWA HAKKO KOGYO KK.	PA	
		XX Handa H, Yamaguchi Y;	Handa H,	
		XX PI 2002-698673/75.	PI	
		XX DR 2002-698673/75.	DR	
		XX PT Non-infective cell-requiring method of searching for hepatitis D remedies in a system containing e.g. polypeptide binding to RNA Polymerase II with measuring of binding level for indication.	PT	
		XX PS Claim 5; SEQ ID NO 7; 84PP; Japanese.	PS	
		XX CC The present invention relates to a method for searching hepatitis D remedies containing e.g. a hepatitis D virus antigen (HDV antigen) and RNA polymerase II, measuring the binding level of HDV antigen binding to RNA polymerase II, and comparing with a control for selection of a compound inhibiting the binding. The method is for screening remedies for hepatitis D including for hepatitis virus D accompanying hepatitis B, such as gene expression promoters applicable in regeneration medicine for treating organs or tissues. The present sequence is a HDV antigen sequence.	CC	
		XX CC The present invention relates to a method for searching hepatitis D remedies adding a test compound to a system containing e.g. a hepatitis D virus antigen (HDV antigen) and RNA polymerase II, measuring the binding level of HDV antigen binding to RNA polymerase II, and comparing with a control for selection of a compound inhibiting the binding. The method is for screening remedies for hepatitis D including for hepatitis virus D accompanying hepatitis B, such as gene expression promoters applicable in regeneration medicine for treating organs or tissues. The present sequence is a HDV antigen sequence.	CC	
		XX SQ Sequence 42 AA;	SQ	
		XX Query Match 25.0%; Score 5; DB 5; Length 42; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 0;	Query Match	
		XX Qy 1 PRGAP 5	Qy	
		XX Db 14 PRGAP 18	Db	
		XX DT 23-MAY-2000 (first entry)	DT	
		XX DE Xenopus thrombospondin 4 trimerisation domain.	DE	
		XX XX Thrombospondin 4; TSP4; KDEL receptor inhibitor; heat shock protein; immune response; oligomerisation domain; neoplasia; sarcoma; lymphoma; leukaemia; melanoma; carcinoma; glioblastoma; astromyoma; oncogene; infectious disease; allergy; autoimmune disease.	XX	
		XX OS Xenopus SP.	OS	
		XX PN WO200006729-A1.	PN	
		XX PD 10-FEB-2000.	PD	
		XX PP 28-JUL-1999; 99WO-US017147.	PP	
		RESULT 24		
		AAW57222		
		ID AAW57222 standard; protein; 44 AA.		
		XX		

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 PR 29-JUL-1998; 98US-00124671.
 XX
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES .
 XX
 PT
 XX
 INVENTION Inhibitors of the KDEL receptor which comprises an oligomerization domain useful for promoting secretion of proteins which are normally retained within the cell. The patent discloses the use of KDEL receptor inhibitor to promote secretion of proteins that are normally retained within the cell such as heat shock proteins by inhibiting KDEL receptor-mediated return of protein complexes to endoplasmic reticulum. This makes the secreted heat shock proteins more accessible to the immune system and improves immune response to a target antigen. The inhibitor protein comprises several subunits where each subunit comprises an oligomerisation domain and has at its carboxy terminus a region which binds to a KDEL receptor. The target antigen may be associated with diseases including neoplasia such as sarcoma, lymphoma, leukemia, carcinoma, glioblastoma and astrocytoma, with defective tumour suppressor genes, oncogenes, infectious diseases, allergy or autoimmune diseases. The present sequence is Xenopus thrombospondin 4 (XSP4) trimerisation domain. Oligomers formed via oligomerisation domain of XSP4 are used to produce high avidity binding protein which bind to KDEL receptor

Sequence 46 AA;
 SQ

Query Match 25.0%; Score 5; DB 3; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETMFL 20
 Db 31 ETMFL 35

RESULT 26 AAM21142
 ID AAM21142 standard; protein; 46 AA.
 XX
 AC
 XX
 DT 12-OCT-2001 (first entry)
 Peptide #2576 encoded by probe for measuring cervical gene expression.
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 OS Homo sapiens .
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-PFB-2000; 20000US-0180312P.
 PR 26-MAY-2000; 20000US-0207456P.
 PR 30-JUN-2000; 20000US-00608408.
 PR 04-FEB-2000; 20000US-0180312P.
 PR 26-MAY-2000; 20000US-0207456P.
 PR 03-AUG-2000; 20000US-00632366.
 PR 21-SEP-2000; 20000US-0234587P.
 PR 27-SEP-2000; 20000US-0236359P.
 PR 04-OCT-2000; 20000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PR 30-JAN-2001; 2001WO-US000670.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53 .

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

Claim 27; SEQ ID NO 25968; 487pp; English.

PS XX
 CC The present invention relates to human single exon nucleic acid probes (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SNPs are derived from human HeLa cells. The SNPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 46 AA;

Query Match 25.0%; Score 5; DB 4; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QMLET 17
 Db 32 QMLET 36

RESULT 27 AAM15409
 ID AAM15409 standard; protein; 46 AA.
 XX
 AC AAM15409;
 XX
 DT 12-OCT-2001 (first entry)
 Peptide #1843 encoded by probe for measuring cervical gene expression.
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.
 XX
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-PFB-2000; 20000US-0180312P.
 PR 26-MAY-2000; 20000US-0207456P.
 PR 30-JUN-2000; 20000US-00608408.
 PR 03-AUG-2000; 20000US-00632366.
 PR 21-SEP-2000; 20000US-0234587P.
 PR 27-SEP-2000; 20000US-0236359P.
 PR 04-OCT-2000; 20000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PR 30-JAN-2001; 2001WO-US000670.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53 .

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.

Claim 27; SEQ ID NO 20235; 487pp; English.

PS XX
 CC The present invention relates to human single exon nucleic acid probes (SENP; see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SNPs are derived from human HeLa cells. The SNPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX

CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 46 AA;

Query Match 25.0%; Score 5; DB 4; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGAPM 6
 Db 20 RGAPM 24

RESULT 28

ID ABB43459 standard; peptide; 46 AA.

XX AC ABB43459;

XX DT 04-FEB-2002 (first entry)

XX Peptide #10965 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PP 09-AUG-2001.

XX PR 30-JAN-2001; 2001WO-US000669.

XX DR 09-AUG-2001.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX DR WPI; 2001-483447/52.

XX XX Query Match 25.0%; Score 5; DB 4; Length 46;

CC Best Local Similarity 100.0%; Pred. No. 2.5e+02;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ Sequence 46 AA;

PS Claim 27; SEQ ID NO 36094; 639bp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human foetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

Qy 13 QMLET 17
 Db 32 QMLET 36

RESULT 29

ID ABB34414

XX standard; peptide; 46 AA.

AC ABB34414;

XX DT 04-FEB-2002 (first entry)

XX Peptide #1920 encoded by human foetal liver single exon probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PP 09-AUG-2001.

XX PR 30-JAN-2001; 2001WO-US000669.

XX DR 09-AUG-2001.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX DR WPI; 2001-483447/52.

XX XX Query Match 25.0%; Score 5; DB 4; Length 46;

CC Best Local Similarity 100.0%; Pred. No. 2.5e+02;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ Sequence 46 AA;

PS Claim 27; SEQ ID NO 36094; 639bp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human foetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

Qy 13 QMLET 17
 Db 32 QMLET 36

RESULT 29

ID ABB34414

XX standard; peptide; 46 AA.

AC ABB34414;

XX DT 04-FEB-2002 (first entry)

XX Peptide #1920 encoded by human foetal liver single exon probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PP 09-AUG-2001.

XX PR 30-JAN-2001; 2001WO-US000669.

XX DR 09-AUG-2001.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX DR WPI; 2001-483447/52.

XX XX Query Match 25.0%; Score 5; DB 4; Length 46;

CC Best Local Similarity 100.0%; Pred. No. 2.5e+02;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC SQ Sequence 46 AA;

PS Claim 27; SEQ ID NO 36094; 639bp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human foetal liver. The

CC present sequence is a peptide encoded by a single exon nucleic acid probe

CC of the invention. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

PS Query Match 25.0%; Score 5; DB 4; Length 46;

XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 46 AA;

Qy 13 QMLET 17
 Db 32 QMLET 36

RESULT 29

ID ABB34414

XX standard; peptide; 46 AA.

AC ABB34414;

XX DT 04-FEB-2002 (first entry)

XX Peptide #1920 encoded by human foetal liver single exon probe.

XX KW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PP 09-AUG-2001.

XX PR 30-JAN-2001; 2001WO-US000669.

XX DR 09-AUG-2001.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

DE Peptide #1934 encoded by probe for measuring placental gene expression.
 XX Probe; microarray; human; Placenta; antenatal diagnosis;
 KW genetic disorder.
 XX OS Homo sapiens.

XX WO200157272-A2.

XX PD 09-AUG-2001.
 XX

XX PF 30-JAN-2001; 2001WO-US000663.

XX PS 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-00632346.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236559P.
 PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human Placenta.
 XX

XX PS Claim 27; SEQ ID NO 28166; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENPs; see AAI31315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders

XX SQ Sequence 46 AA;

XX Query Match 25.0%; Score 5; DB 4; Length 46;
 PT Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 PT Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 13 QMLET 17
 XX Db 32 QMLET 36
 XX RESULT 32
 CC ABB29251 standard; peptide; 46 AA.
 CC ID ABB29251
 CC AC ABB29251;
 XX DT 01-FEB-2002 (first entry)
 XX DE Peptide #1902 encoded by breast cell single exon nucleic acid probe.
 XX Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer.
 XX Homo sapiens.
 XX OS WO200157271-A2.

XX PN 09-AUG-2001.
 XX PD 09-AUG-2001.
 XX XX

XX XX 30-JAN-2001; 2001WO-US000662.
 XX AC AAM37347;
 XX DT 17-OCT-2001 (first entry)

XX DE Peptide #11384 encoded by probe for measuring placental gene expression.
 XX Probe; microarray; human; Placenta; antenatal diagnosis;
 KW genetic disorder.
 XX OS Homo sapiens.

XX PN WO200157272-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000663.
 XX PS 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632346.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236559P.
 PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR 2001-496933/54.

XX PT New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.

XX Claim 27; SEQ ID NO 12219; 327pp + Sequence Listing; English.
 XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic DNA. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 46 AA;

Query Match 25.0%; Score 5; DB 4; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RGAPM 6
 Db 20 RGAPM 24

RESULT 33
 ABB19826
 ID ABB19826 standard; protein: 46 AA.
 XX Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX Homo sapiens.
 OS Homo sapiens.
 DT 23-JAN-2002 (first entry)
 XX Protein #1825 encoded by probe for measuring heart cell gene expression.
 XX
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX WO200157274-A2.
 PN WO200157274-A2.
 XX PD 09-AUG-2001.
 XX 30-JAN-2001; 2001WO-US000666.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-02344897P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

(MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI XX DR; WPI; 2001-488900/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX PA Example 4; SEQ ID NO 27305; 658pp + Sequence Listing; English.
 PS XX

The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX Sequence 46 AA;
 PS

Claim 15; SEQ ID NO 21596; 530pp; English.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR; WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.
 XX PA

Query Match 25.0%; Score 5; DB 4; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGAPM 6
 Db 20 RGAPM 24

AC ABG58835;
 XX DT 25-FEB-2003 (first entry)
 XX Human liver peptide, SEQ ID No 37483.
 KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 XX OS Homo sapiens.
 XX PN WO200157273-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JUN-2001; 2001WO-US000664.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-020456P.
 XX PR 30-JUN-2000; 2000US-0608408.
 XX PR 03-AUG-2000; 2000US-0662366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-0234659P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR 2001-488B98/53.
 XX WPI; 2001-488B98/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.
 PT Claim 27; SEQ ID NO 37483; 650pp; English.

XX The invention relates to a single exon nucleic acid probe (SBNP) (I) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult liver.
 CC (I) may be used for predicting, measuring and displaying gene expression
 CC in samples derived from human adult liver. The genes identified may be
 CC involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
 CC associated with coronary heart disease. ABG47348-ABG59930 represent human
 CC liver single exon encoded peptides of the invention. Note: The sequence
 CC information for this patent does not appear in the printed specification
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 46 AA;

XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR 2001-483446/52.
 XX PS Example 4; SEQ ID NO 36494; 650pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.
 XX SQ Sequence 46 AA;

XX Query Match 25.0%; Score 5; DB 4; Length 46;
 CC Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QMLET 17
 Db 32 QMLET 36

RESULT 36
 ABG58835
 ID ABG58835 standard; peptide; 46 AA.
 XX DE Human liver peptide, SEQ ID No 27894.
 KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

KW	hypercholesterolaemia; coronary heart disease.	XX	29-JAN-2001; 2001WO-US000661.
OS	Homo sapiens.	PF	29-JAN-2001; 2001WO-US000661.
XX		XX	
PN	WO200157273-A2.	PR	04-FEB-2000; 2000US-0180312P.
XX		PR	26-MAY-2000; 2000US-020746P.
PD	09-AUG-2001.	PR	30-JUN-2000; 2000US-00609408.
XX		PR	03-AUG-2000; 2000US-0063266.
PF	30-JAN-2001; 2001WO-US000664.	PR	21-SEP-2000; 2000US-023467P.
XX		PR	27-SEP-2000; 2000US-023639P.
PR	04-FEB-2000; 2000US-0180312P.	PR	04-OCT-2000; 2000US-023639P.
PR	26-MAY-2000; 2000US-020746P.	XX	04-OCT-2000; 2000GB-0002463.
PR	30-JUN-2000; 2000US-00608408.	PA	(MOLE-) MOLECULAR DYNAMICS INC.
PR	03-AUG-2000; 2000US-00632366.	PI	Penn SG, Hanzel DK, Chen W, Rank DR;
PR	21-SEP-2000; 2000US-023468P.	DR	WPI; 2001-476286/51.
PR	27-SEP-2000; 2000US-023635P.	XX	
PR	04-OCT-2000; 2000GB-00024263.	PT	Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
XX		PT	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	PT	
XX		PT	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;	PS	Claim 27; SEQ ID NO 11910; 322PP; English.
XX		XX	
DR	2001-488898/53.	CC	The present invention relates to novel single exon nucleic acid probes (see AI0010-AII0067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosticating diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, breast disease and non-carcinoma tumours. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX		XX	
PT	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.	CC	
PT	Claim 27; SEQ ID NO 27894; 658PP; English.	PS	
XX		XX	
CC	The invention relates to a single exon nucleic acid probe (SENTP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinæmia, hyperlipidaemia and hypercholesterolemia which is associated with coronary heart disease. ABG4/348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at specification ftp.wipo.int/pub/published_pct_sequences	XX	
XX		CC	
SQ	Sequence 46 AA:	CC	
XX		CC	
Query Match	25.0% Score 5; DB 4; Length 46;	RESULT 39	
Best Local Similarity	100.0% Pred. No. 2.5e+02;	ABG46722	
Matches	Mismatches 0; Indels 0; Gaps 0;	ID	ABG46722 standard; peptide; 46 AA.
Qy	2 RGAPM 6	XX	
Db	20 RGAPM 24	AC	ABG46722;
		XX	
		DT	19-AUG-2002 (first entry)
		DE	Human peptide encoded by genome-derived single exon probe SEQ ID 35887.
		XX	
		KW	Human; single exon probe; asthma; lung cancer; COPD; ILD;
		KW	chronic obstructive pulmonary disease; interstitial lung disease;
		KW	familial idiopathic pulmonary fibrosis; neurofibromatosis;
		KW	tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
		KW	Hermannsky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
		KW	pulmonary histiocytosis lymphangiolieomyomatosis; Kartagener syndrome;
		KW	pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
		KW	primary ciliary dyskinesia; pulmonary hypertension;
		KW	hyaline membrane disease.
		CS	Homo sapiens.
		XX	
		PN	WO200186003-A2.
		XX	
		PD	15-NOV-2001.
		XX	

PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-0063236.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 Penn SG, Hanzel DK, Chen W, Rank DR;
 PT
 XX
 DR; 2002-114183/15.
 XX
 Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 Claim 27; SEQ ID NO 35887; 634pp; English.
 XX
 The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements, or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labelled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labelled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA, and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 CC histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis,
 CC Kartagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp://wipo.int/pub/published_pct_sequences
 XX
 Sequence 46 AA;
 Query Match 25.0% Score 5; DB 5; Length 46;
 Best Local Similarity 100.0% Pred. No. 2.5e02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	13 QMLET 17
Dy	32 QMLET 36

RESULT 40
 ABG37192

ID ABG37192 standard; peptide; 46 AA.
 XX
 AC ABG37192;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DB Human peptide encoded by genome-derived single exon probe SEQ ID 26857.
 XX
 KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangiomyomatosis; Kartagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.
 XX
 Homo sapiens.
 OS
 XX
 PN WO200186003-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-0063236.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 Penn SG, Hanzel DK, Chen W, Rank DR;
 PT
 XX
 WPI; 2002-114183/15.
 XX
 Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 Claim 27; SEQ ID NO 26857; 634pp; English.
 XX
 The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements, or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC ; the novel set of probes which hybridise at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labelled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridisation of detectably
 CC labelled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridisation to a single exon probe,
 CC microarrays having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 46 AA;

Query Match 25.0%; Score 5; DB 5; Length 46;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 RGAPM 6
 Db 20 RGAPM 24

RESULT 41

ABB38152

standard; peptide; 47 AA.

XX DT 04-FEB-2002 (first entry)
 AC ABB38152;
 XX DT 04-FEB-2002 (first entry)

Peptide #5658 encoded by human foetal liver single exon probe.

Human; foetal liver; gene expression; single exon nucleic acid probe.

XX KW Homo sapiens.

OS Homo sapiens.

XX PN WO200157277-A2.

XX PD 09-AUG-2001.

XX PP 09-AUG-2001; 2001WO-US000663.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00603408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234667P.

XX PR 27-SEP-2000; 2000US-023659P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR.

XX XX DR; 2001-488897/53.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.

XX BS Claim 27; SEQ ID NO 31849; 654pp; English.

XX CC The present invention relates to single exon nucleic acid probes (SENPs; see ARI3115-AI157516). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.

XX SQ Sequence 47 AA;

PT Gene expression in human fetal liver.

XX PS Claim 27; SEQ ID NO 30787; 630pp + Sequence Listing; English.

XX CC The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human foetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX SQ Sequence 47 AA;

PT Query Match 25.0%; Score 5; DB 4; Length 47;

XX PS Best Local Similarity 100.0%; Pred. No. 2.6e+02;

XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 1 PRGAP 5
 13 PRGAP 17

RESULT 43

ABB23358

standard; protein: 47 AA.

XX AC ABB23358;

XX DT 23-JAN-2002 (first entry)

XX Protein #5357 encoded by probe for measuring heart cell gene expression.

DE XX

KW Human; gene expression; heart; microarray; vascular system;

KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease.

XX

Homo sapiens.

CS XX

WO200157274-A2.

XX

PN PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000666.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234667P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-0024263.

XX

(MOLE-) MOLECULAR DYNAMICS INC.

PA XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WBI; 2001-488899/53.

XX

Single exon nucleic acid probes for analyzing gene expression in human hearts.

XX

PT Claim 15; SEQ ID NO 25128; 530pp; English.

XX

CC The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see CC ABA21515-ABA4130). The present sequence is a protein encoded by one such CC probe. The probes may be used for predicting, measuring and displaying CC gene expression in samples derived from the human heart via microarrays.

CC By measuring gene expression, the probes are useful for predicting, CC diagnosing, grading, staging, monitoring and prognosis diseases of the CC human heart and vascular system e.g. cardiovascular disease, CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The CC sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp://wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 47 AA;

Qy	PRAP 5	PRAP 17
Best Local Matches	25.0% ; Score 5 ; DB 4 ; Length 47 ; 100.0% ; Pred. No. 2.6e+02 ; 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0	
Db	13	

RESULT 44

ID	AM71301 standard; protein; 47 AA.
XX	AM71301;
XX	06-NOV-2001 (first entry)
DE	Human bone marrow expressed probe encoded protein SEQ ID NO: 31607.
XX	
KW	Human; bone marrow expressed exon; gene expression analysis; probe;
KW	microarray; cancer; leukaemia; lymphoma; myeloma.
XX	
OS	Homo sapiens.

PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0150312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0008408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-024687P.
 PR 27-SEP-2000; 2000US-0246359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hamzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488300/53.
 XX
 Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX
 PS Example 4: SEQ ID NO 31607; 658pp + Sequence Listing; English.
 XX
 The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX
 SQ Sequence 47 AA;
 Query Match 25.00%; Score 5; DB 4; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 YY 1 PRGAP 5
 Db 13 PRGAP 17
 RESULT 45
 AAM58788
 ID AAM58788 standard; protein; 47 AA.
 XX
 AC AAM58788;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30893
 XX
 KW Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0160408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234587P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-433446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human brains.

XX Example 4; SEQ ID NO 30893; 650pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention

XX Sequence 47 AA;

Query Match 25.0%; Score 5; DB 4; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGAP 5
 Db 13 PRGAP 17

RESULT 47
 ABG53012 standard; peptide; 47 AA.

XX ABG53012;
 AC ABG53012;
 DT 25-FEB-2003 (first entry)
 DE Human liver peptide, SEQ ID NO 31660.
 KW Human; liver; cirrhosis; hyperlipoproteinæmia; hyperlipidaemia;
 KW hypercholesterolaemia; coronary heart disease.
 XX OS Homo sapiens.
 PN WO200157273-A2.

XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000664.

XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488898/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

XX Claim 27; SEQ ID NO 311660; 650pp; English.

CC The invention relates to a single exon nucleic acid probe (SENPs) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high

CC stringency to a nucleic acid molecule expressed in the human adult liver.

CC (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis,

CC hyperlipoproteinæmia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG4748-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

CC Query Match 25.0%; Score 5; DB 4; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGAP 5
 Db 13 PRGAP 17

RESULT 47
 ABG41101 standard; peptide; 47 AA.

XX ABG41101;
 AC ABG41101;
 XX 19-AUG-2002 (first entry)

DS Human peptide encoded by genome-derived single exon probe SEQ ID 30766.

XX Human: single exon probe; asthma; lung cancer; COPD; TLD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
 KW tuberculous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangiomyomatosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW hyaline membrane disease.

XX Homo sapiens.

OS XX WO200186003-A2.
 PN XX ED 15-NOV-2001.
 XX PF 30-JAN-2001; 2001WO-US000665.

XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2002-114183/15.

XX Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

XX PS Claim 27; SEQ ID NO 30766; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their

complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes ; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a sample collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labelled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences mentioned in the specification, or encoded by the probe/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, sarcoidosis, Gaucher's disease, Niemann-Pick disease, Pulmonary histiocytosis, lymphangioleiomomtosis, pulmonary alveolar proteinosis, Karshner syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 47 AA;

Query Match	25.0%	Score 5;	DB 5;	Length 47;
Best Local Similarity	100.0%;	Pred. No. 2.6e+02;		
Matches	5;	Mismatches	0;	Indels
Qy	1 PRGAP 5			
Db	13 PRGAP 17			

RESULT 48

ID	ABG19401	standard; protein; 50 AA.
ID	ABG19401	standard; protein; 54 AA.
XX	AC	ABG19401;
XX	DT	18-FEB-2002 (first entry)
XX	DE	Novel human diagnostic protein #19392.
XX	KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; Homo sapiens.
XX	PN	WO200175067-A2.
XX	PD	11-OCT-2001.
XX	PP	30-MAR-2001; 2001WO-US008631.
XX	PR	31-MAR-2000; 2000US-00540217.
PR	23-AUG-2000; 2000US-00649167.	
XX	PA	(HYSEQ-) HYSEQ INC.
XX	PR	Dirmancic RT, Liu C, Tang YT;
PI	PR	01-APR-1999; 99US-0127462P.

XX	WPI; 2001-639362/73.
DR	N-PSDB; AAS8388.

XX	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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XX	Claim 20; SEQ ID NO 49760; 103pp; English.
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PS	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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XX Sequence 50 AA;

Query	Match	25.0%;	Score 5;	DB 4;	Length 50;
Best Local Similarity	100.0%;	Pred. No. 2.7e+02;	Mismatches	0;	Indels
Matches	5;	Conservative	0;	Gaps	0;

Qy

1 PRGAP 5

|||||

Db

16 PRGAP 20

XX

RESULT 49

AAG5791.0	standard; protein; 54 AA.
ID	AAG57910.

XX

AAG57910;

XX

18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 74690.

XX KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX KW Arabidopsis thaliana.

XX OS EP1033405-A2.

XX PD 06-SEP-2000.

XX XX 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121823P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123545P.

PR 23-MAR-1999; 99US-0125789P.

PR 25-MAR-1999; 99US-0126244P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR	06-APR-1999;	99US-0128234P.	PR	19-JUL-1999;	99US-0144332P.
PR	08-APR-1999;	99US-0128714P.	PR	19-JUL-1999;	99US-0144333P.
PR	16-APR-1999;	99US-0129845P.	PR	19-JUL-1999;	99US-0144334P.
PR	19-APR-1999;	99US-0130077P.	PR	19-JUL-1999;	99US-0144335P.
PR	21-APR-1999;	99US-0130449P.	PR	20-JUL-1999;	99US-0144332P.
PR	23-APR-1999;	99US-0130510P.	PR	20-JUL-1999;	99US-0144632P.
PR	23-APR-1999;	99US-0130891P.	PR	20-JUL-1999;	99US-0144894P.
PR	28-APR-1999;	99US-0131499P.	PR	21-JUL-1999;	99US-0144846P.
PR	30-APR-1999;	99US-0132048P.	PR	21-JUL-1999;	99US-0145068P.
PR	30-APR-1999;	99US-0132407P.	PR	21-JUL-1999;	99US-0145088P.
PR	04-MAY-1999;	99US-0132484P.	PR	22-JUL-1999;	99US-0145055P.
PR	05-MAY-1999;	99US-0132485P.	PR	22-JUL-1999;	99US-0145097P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145099P.
PR	06-MAY-1999;	99US-0132487P.	PR	23-JUL-1999;	99US-0145122P.
PR	07-MAY-1999;	99US-0132488P.	PR	23-JUL-1999;	99US-0145125P.
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Query Match Best Local Similarity Score 5; DB 3; Length 54;
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RESULT 50
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 XX DT 18-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 80105.
 XX KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX OS Arabidopsis thaliana.
 XX PN EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PF 25-FEB-2000; 20000BP-00301039.
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WPI ; 2003-521747/49.
 New bone metabolism-related proteins and nucleic acids encoding the proteins, useful in the activation process of the osteoblasts and induction of successive recruitment of the osteoclasts in bone remodeling processes.
 Example 7; Fig 6; 31pp; English.

The invention describes an isolated murine or human polypeptide (I). The nucleic acid is useful for suppressing or strengthening the promotion of differentiation of osteoblast, induction of morphological change of a cell, or expression of an esterase activity. The antibody is useful for neutralising a function or an activity of the polypeptide. Detecting a function or an activity of the polypeptide or the nucleic acid is useful for screening or identifying compounds, e.g. pharmaceutical compounds, which modulate the function or activity of the polypeptide. The identified compounds are valuable for selling. The polypeptides are also useful in the activation process of the osteoblasts and induction of successive recruitment of the osteoclasts in bone remodeling process. The polypeptides and nucleic acids are useful in studies on pathological states, diagnostics, therapeutic and prophylactic treatment, and research and development of pharmaceuticals for diseases such as osteoporosis, osteomalacia or hypercalcaemia. This is the amino acid sequence of mouse osteoblast differentiation promoting factor (OBDFP) fragment used in comparison with known enzymes during the functional analysis of OBDFP.

Sequence 54 AA:

Query Match 25.0%; Score 5; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 2.9e+02; Mismatches 0; Indels 0; Gaps 0;

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AC AAG60769;
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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 78752.

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OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.

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PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161393P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161394P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161395P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161932P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161933P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162142P.
PR	05-AUG-1999;	99US-0147192P.	PR	22-OCT-1999;	99US-0160981P.
PR	06-AUG-1999;	99US-0147303P.	PR	22-OCT-1999;	99US-016099P.
PR	06-AUG-1999;	99US-0147416P.	PR	25-OCT-1999;	99US-0161404P.
PR	09-AUG-1999;	99US-0147417P.	PR	25-OCT-1999;	99US-0161405P.
PR	09-AUG-1999;	99US-0147933P.	PR	26-OCT-1999;	99US-0161392P.
PR	10-AUG-1999;	99US-0148171P.	PR	26-OCT-1999;	99US-0161393P.
PR	11-AUG-1999;	99US-0148319P.	PR	28-OCT-1999;	99US-0161394P.
PR	12-AUG-1999;	99US-0148341P.	PR	28-OCT-1999;	99US-0148565P.
PR	13-AUG-1999;	99US-0148684P.	PR	20-AUG-1999;	99US-0148684P.
PR	13-AUG-1999;	99US-0147973P.	PR	20-AUG-1999;	99US-0149722P.
PR	16-AUG-1999;	99US-0149929P.	PR	23-AUG-1999;	99US-0149902P.
PR	17-AUG-1999;	99US-0149915P.	PR	23-AUG-1999;	99US-0149930P.
PR	18-AUG-1999;	99US-0149426P.	PR	25-AUG-1999;	99US-0150566P.
PR	20-AUG-1999;	99US-0149722P.	PR	20-SEP-1999;	99US-0150844P.
PR	20-AUG-1999;	99US-0149733P.	PR	27-AUG-1999;	99US-0151065P.
PR	23-AUG-1999;	99US-0149929P.	PR	27-AUG-1999;	99US-0151066P.
PR	23-AUG-1999;	99US-0149930P.	PR	30-AUG-1999;	99US-0151080P.
PR	25-AUG-1999;	99US-0151310P.	PR	31-AUG-1999;	99US-0151338P.
PR	01-SEP-1999;	99US-0151330P.	PR	01-SEP-1999;	99US-0152353P.
PR	07-SEP-1999;	99US-0153070P.	PR	10-SEP-1999;	99US-0153070P.
PR	13-SEP-1999;	99US-0153738P.	PR	15-SEP-1999;	99US-0154018P.
PR	15-SEP-1999;	99US-0154039P.	PR	16-SEP-1999;	99US-0154039P.
PR	20-SEP-1999;	99US-0154779P.	PR	22-SEP-1999;	99US-0155139P.
PR	23-SEP-1999;	99US-0155486P.	PR	23-SEP-1999;	99US-0155639P.
PR	28-SEP-1999;	99US-015658P.	PR	28-SEP-1999;	99US-0156596P.
PR	29-SEP-1999;	99US-015693P.	PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-015753P.	PR	06-OCT-1999;	99US-0157865P.
PR	14-OCT-1999;	99US-015829P.	PR	08-OCT-1999;	99US-0158322P.
PR	14-OCT-1999;	99US-0158369P.	PR	12-OCT-1999;	99US-0158331P.
PR	13-OCT-1999;	99US-0159294P.	PR	13-OCT-1999;	99US-0159338P.
PR	13-OCT-1999;	99US-0159295P.	PR	18-OCT-1999;	99US-0159584P.
PR	14-OCT-1999;	99US-0159339P.	PR	21-OCT-1999;	99US-0160741P.
PR	14-OCT-1999;	99US-0159330P.	PR	21-OCT-1999;	99US-0160767P.
PR	14-OCT-1999;	99US-0159331P.	PR	21-OCT-1999;	99US-0160768P.
PR	14-OCT-1999;	99US-0159332P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-OCT-1999;	99US-0160980P.	PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.	PR	22-OCT-1999;	99US-0160980P.

Query Match 25.0% Score 5; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QMLET 17
Db 48 QMLET 52

RESULT 53
ABP6407
ID ABP6407 standard; protein; 57 AA.

XX ABP6407;
XX 04-NOV-2002 (first entry)
DE Human ORF977.

XX Cytostatic; Cardiант; Anti-allergic; Immunosuppressive; Vulnerary;

KW Antiinflammatory; Gene therapy; human; ORFX; atherogenic; platelet; human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque; cancer; cardiovascular disease; allergy; autoimmune disease; wound healing; blood coagulation disorder; inflammatory disorder. Homo sapiens.

XX OS XX

US2002082206-A1.

XX DT 27-JUN-2002.

XX DE 30-MAY-2001; 2001US-00867550.

XX EP 30-MAY-2000; 2000US-0208427P.

XX PR 27-JUN-2002.

XX PR 30-MAY-2001; 2001US-00867550.

XX PR 30-MAY-2000; 2000US-0208427P.

XX PR 27-JUN-2002.

XX PI Leach MD, Mehraian F, Conley PB, Topper JN, Law D; DR WPI; 2002-626554/67.

XX N-PSDB; ABQ99170.

XX Claim 10; SEQ ID NO 1954; 78pp; English.

The present invention relates to novel human ORFX polypeptides and their coding sequences (ABP63631 and ABQ98194-ABQ9267). The sequences were discovered in human atherogenic cells, in particular in platelets and human umbilical vein endothelial cells (HUVEC) and are expressed in many other tissues as well. Atherogenic cells are cells which have the potential to develop atherosclerotic plaques. The ORFX polypeptides and nucleic acids are useful for treating or preventing a pathological

condition associated with an ORFX-associated disorder, e.g. cancer, cardiovascular disease, allergy, autoimmune disease, wound healing, coagulation disorders or inflammatory disorders. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/sequence.html?DocID=20020082206

Sequence 57 AA:

Qy	11 VCQML 15	22 VCQML 26
Db		

RESULT 54

AAU46690
ID AAU46690 standard; protein; 62 AA.

XX AAU46690;

XX DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #7586.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

XX uveitis; endophthalmitis; bone joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

XX dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US012865.

XX PR 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX PA (CORTI-CORIXA CORP.

XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PT L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX DR 2001-616774/71.

XX WPI; N-PSDB; AA559534.

PT Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

XX Example 1: SEQ ID NO 7885; 106pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and

therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

Sequence 62 AA:

Qy	25.0%; Score 5; DB 5; Length 57;	Best Local Similarity 100.0%; Pred. No. 3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DB 4; Score 5; DB 4; Length 62; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db			

RESULT 55

ABM43209
ID ABM43209 standard; protein; 62 AA.

XX AC ABM43209;

XX DT 20-OCT-2003 (first entry)

XX Propionibacterium acnes predicted ORF-encoded polypeptide #7885 . DE Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;

XX immunostimulant; immune response; vaccine.

XX Propionibacterium acnes.

XX OS Propionibacterium acnes.

XX PN WO2003033515-A1.

XX PR 24-APR-2003.

XX PF 11-OCT-2002; 2002WO-US032727.

XX PR 15-OCT-2001; 2001US-00978825.

XX PA (CORI-CORIXA CORP.

XX PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A,

XX PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;

XX PI Barth B, Valilieve-Douglas J;

XX DR WPI; 2003-381789/36.

XX N-PSDB; AC64463.

XX New Propionibacterium acnes polypeptides and polymucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

XX Example 1: SEQ ID NO 7885; 1481pp; English.

CC The invention relates to an isolated polymucleotide (AC64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to CC polymucleotides encoded by the polymucleotides (ABM3564-ABM64516) and to CC immunogenic fragments of P. acnes polypeptides. The invention CC additionally encompasses expression vectors and host cells comprising a CC polymucleotide of the invention; antibodies against polypeptides of the CC invention; fusion proteins comprising a polypeptide of the invention; a CC method for stimulating an immune response specific for a P. acnes CC polypeptide and an isolated T cell population comprising T cells prepared CC via this method; a vaccine composition (comprising P. acnes polypeptides, CC polymucleotides, antibodies, fusion proteins, T cell populations, or CC antigen-presenting cells that express the polypeptide); a method and kit CC for detecting or determining the presence or absence of P. acnes in a CC patient; and a method for inhibiting the development of P. acnes in a CC patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion CC proteins, T cell populations or antigen-presenting cells that express the CC polypeptides are useful for diagnosing, preventing or treating acne

CC vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes poly nucleotides of the invention. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX

Sequence 62 AA;

Qy	1	PRGAP 5	Score 5;	DB 6;	Length 62;
Db	8	PRGAP 12	Best Local Similarity 100.0%;	Pred. No. 3.3e+02;	Mismatches 0;
			Matches 5	Conservative 0;	Indels 0;
				Gaps 0;	

RESULT 56
DT 18-OCT-2000 (First entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 78751.

XX KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

PD 06-SEP-2000.

XX PP 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0127834P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0128845P.

PR 19-APR-1999; 99US-0132048P.

PR 21-APR-1999; 99US-0130077P.

PR 04-MAY-1999; 99US-012484P.

PR 05-MAY-1999; 99US-0130510P.

PR 23-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-011449P.

PR 30-APR-1999; 99US-0132863P.

PR 04-MAY-1999; 99US-0134256P.

PR 05-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-014221P.

PR 14-MAY-1999; 99US-014370P.

PR 18-MAY-1999; 99US-0134768P.

PR 19-MAY-1999; 99US-0134941P.

storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704

XX Sequence 63 AA;

Query Match 25.0%; Score 5; DB 8; Length 63;

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGAP 5

Db 15 PRGAP 19

RESULT 58

ABP00767

ID ABP00767 standard; protein; 64 AA.

AC AC

XX

DT 25-JUN-2002 (First entry)

XX DE Human ORFX protein sequence SEQ ID NO:15116.

XX

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; KW degenerative disorder; osteoarthritis; neurodegenerative disorder; KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; KW hypertension; hypothyroidism; cholesterol ester storage disease; KW immune deficiency; immune disorder; infectious disease; KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; KW myasthenia gravis.

XX OS Homo sapiens.

XX PN WC200192523-A2.

XX PD 06-DEC-2001.

XX XX

PF 29-MAY-2001; 2001WO-US1010836.

XX XX

PR 30-MAY-2000; 2000US-0205132P.

PR 29-AUG-2000; 2000US-0228716P.

XX XX

(CFDA-) CURAGEN CORP.

XX PI Shimkets RA, Leach MD;

XX DR WPI: 2002-106308/14.

DR N-FSDB; ABN16519.

XX PS Disclosure; SEQ ID NO 1516; 1037bp; English.

XX XX

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX

proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX Polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ	Sequence 64 AA;	Query Match 1 PRGAP 5	Score 25.0%; DB 5; Length 64;
		Best Local Similarity 100.0%; Pred. No. 3.3e+02;	
		Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		Db 19 PRGAP 23	
<hr/>			
RESULT 59	Query Match 1 PRGAP 5	Score 25.0%; DB 5; Length 64;	
	ID AAG61788	Best Local Similarity 100.0%; Pred. No. 3.3e+02;	
	XX	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
	AC AAG61788;		
	XX	DT 18-OCT-2000 (first entry)	
	DE Arabidopsis thaliana protein fragment SEQ ID NO: 80257.		
	XX	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; KW termination sequence.	
	OS Arabidopsis thaliana.		
	XX	PN EP1033405-A2.	
	XX	PD 06-SEP-2000.	
	XX	PP 25-FEB-2000; 2000EP-00301439.	
	XX	PR 25-FEB-1999; 99US-0121825P.	
	PR 05-MAR-1999; 99US-0123540P.		
	PR 09-MAR-1999; 99US-0125788P.		
	PR 23-MAR-1999; 99US-0126264P.		
	PR 25-MAR-1999; 99US-0127155P.		
	PR 29-MAR-1999; 99US-0127462P.		
	PR 01-APR-1999; 99US-0127462P.		
	PR 06-APR-1999; 99US-0128234P.		
	PR 08-APR-1999; 99US-0128714P.		
	PR 16-APR-1999; 99US-0129845P.		
	PR 19-APR-1999; 99US-0130077P.		
	PR 21-APR-1999; 99US-013051P.		
	PR 23-APR-1999; 99US-013089P.		
	PR 28-APR-1999; 99US-013144P.		
	PR 30-APR-1999; 99US-013204P.		
	PR 30-APR-1999; 99US-0132407P.		
	PR 04-MAY-1999; 99US-0132484P.		

PR	05-MAY-1999;	99US-0132485P.	PR	22-JUL-1999;	99US-0145087P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145089P.
PR	06-MAY-1999;	99US-0132487P.	PR	22-JUL-1999;	99US-014519P.
PR	07-MAY-1999;	99US-0132863P.	PR	23-JUL-1999;	99US-014514P.
PR	11-MAY-1999;	99US-0134256P.	PR	23-JUL-1999;	99US-0145216P.
PR	14-MAY-1999;	99US-0134218P.	PR	23-JUL-1999;	99US-0145224P.
PR	14-MAY-1999;	99US-0134219P.	PR	26-JUL-1999;	99US-0145276P.
PR	14-MAY-1999;	99US-0134221P.	PR	27-JUL-1999;	99US-0145913P.
PR	14-MAY-1999;	99US-0134370P.	PR	27-JUL-1999;	99US-0145918P.
PR	18-MAY-1999;	99US-0134768P.	PR	27-JUL-1999;	99US-0145919P.
PR	19-MAY-1999;	99US-0134941P.	PR	28-JUL-1999;	99US-0145951P.
PR	20-MAY-1999;	99US-0135124P.	PR	02-AUG-1999;	99US-0146386P.
PR	21-MAY-1999;	99US-0135533P.	PR	02-AUG-1999;	99US-0146388P.
PR	04-JUN-1999;	99US-0137502P.	PR	02-AUG-1999;	99US-0146389P.
PR	25-MAY-1999;	99US-0136021P.	PR	03-AUG-1999;	99US-0147038P.
PR	27-MAY-1999;	99US-0136392P.	PR	04-AUG-1999;	99US-0147204P.
PR	28-MAY-1999;	99US-0136782P.	PR	04-AUG-1999;	99US-0147302P.
PR	01-JUN-1999;	99US-0137222P.	PR	05-AUG-1999;	99US-0147192P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147260P.
PR	04-JUN-1999;	99US-0137502P.	PR	06-AUG-1999;	99US-0147303P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147416P.
PR	08-JUN-1999;	99US-0138004P.	PR	09-AUG-1999;	99US-0147493P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147935P.
PR	10-JUN-1999;	99US-0138847P.	PR	10-AUG-1999;	99US-0148171P.
PR	14-JUN-1999;	99US-0138911P.	PR	11-AUG-1999;	99US-0148319P.
PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	17-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139452P.	PR	13-AUG-1999;	99US-014684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139459P.	PR	20-AUG-1999;	99US-014929P.
PR	18-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-014902P.
PR	22-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-014930P.
PR	23-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-015666P.
PR	23-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0156884P.
PR	24-JUN-1999;	99US-0139465P.	PR	27-AUG-1999;	99US-0151065P.
PR	28-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151066P.
PR	29-JUN-1999;	99US-0139817P.	PR	27-AUG-1999;	99US-0151080P.
PR	30-JUN-1999;	99US-0139899P.	PR	30-AUG-1999;	99US-0153303P.
PR	01-JUL-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-015438P.
PR	01-JUL-1999;	99US-0142155P.	PR	01-SEP-1999;	99US-0153930P.
PR	02-JUL-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-015363P.
PR	06-JUL-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0154070P.
PR	08-JUL-1999;	99US-014091P.	PR	13-SEP-1999;	99US-015758P.
PR	09-JUL-1999;	99US-0142220P.	PR	15-SEP-1999;	99US-015458P.
PR	12-JUL-1999;	99US-014287P.	PR	16-SEP-1999;	99US-015596P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0142055P.	PR	05-OCT-1999;	99US-0157753P.
PR	19-JUL-1999;	99US-0143674P.	PR	13-OCT-1999;	99US-0159224P.
PR	19-JUL-1999;	99US-0144330P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144344P.	PR	14-OCT-1999;	99US-0159339P.
PR	19-JUL-1999;	99US-0144086P.	PR	14-OCT-1999;	99US-0158232P.
PR	20-JUL-1999;	99US-0144350P.	PR	12-OCT-1999;	99US-0158369P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144884P.	PR	14-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0144814P.	PR	21-OCT-1999;	99US-016741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145085P.	PR	21-OCT-1999;	99US-0160768P.

Query Match 25.0%; Score 5; DB 5; Length 66;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 30 PRGAP 34

RESULT 61
 ID ADF94733
 XX Hepatitis D virus type III antigen protein fragment, SEQ ID 8.
 AC ADF94733;
 XX Virucide; hepatitis D virus antigen; HDV antigen; RNA polymerase II.

DT 26-FEB-2004 (first entry)
 XX DE Hepatitis D virus type III antigen protein fragment, SEQ ID 8.
 XX KW Virucide; hepatitis D virus antigen; HDV antigen; RNA polymerase II.

XX OS Hepatitis D virus.

EN WO200268655-A1.

XX PD 06-SEP-2002.

XX BP 27-FEB-2002; 2002WO-JP001817.

XX PR 27-FEB-2001; 2001JP-00053163.

PA (CIRCLE PROMOTION SCI & ENG.
 PA (KYOWA HAKKO KOGYO KK.
 PI Handa H, Yamaguchi Y;
 XX DR WPI; 2002-698673/75.

XX PT Non-infective cell-requiring method of searching for hepatitis D remedies
 PT in a system containing e.g. polypeptide binding to RNA polymerase II with
 PT measuring of binding level for indication.

XX SQ Sequence 66 AA;

PR 27-FEB-2001; 2001JP-00053163.

PA (CIRCLE PROMOTION SCI & ENG.
 PA (KYOWA HAKKO KOGYO KK.
 PI Handa H, Yamaguchi Y;
 XX DR WPI; 2002-698673/75.

CC The present invention relates to a method for searching hepatitis D remedies. The method comprises adding a test compound to a system containing e.g. a hepatitis D virus antigen (HDV antigen) and RNA polymerase II, measuring the binding level of HDV antigen binding to RNA polymerase II, and comparing the method with a control for selection of a compound inhibiting the binding. The method is for screening remedies for hepatitis D including for hepatitis virus D accompanying hepatitis B, such as gene expression promoters applicable in regeneration medicine for treating organs or tissues. The present sequence is a HDV antigen sequence.

CC Sequence 66 AA;

Query Match 25.0%; Score 5; DB 5; Length 66;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 30 PRGAP 34

RESULT 62
 ID AAM83752
 XX Hepatitis D virus type III antigen protein fragment, SEQ ID 8.
 AC AAM83752

DT 07-NOV-2001 (first entry)
 XX Human immune/haematopoietic antigen SEQ ID NO:11345.
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cycostatic; gene therapy; vaccine; metastasis.
 XX
 OS Homo sapiens.
 XX WO200157182-A2.
 XX PR 09-AUG-2001.
 XX PR 17-JAN-2001; 2001WO-US001354.
 XX PR 31-JAN-2000; 2000US-0179065P.
 XX PR 04-FEB-2000; 2000US-0180628P.
 XX PR 24-FEB-2000; 2000US-0184664P.
 XX PR 02-MAR-2000; 2000US-0186350P.
 XX PR 16-MAR-2000; 2000US-0189374P.
 XX PR 17-MAR-2000; 2000US-019076P.
 XX PR 18-APR-2000; 2000US-019123P.
 XX PR 19-MAY-2000; 2000US-020515P.
 XX PR 07-JUN-2000; 2000US-0209467P.
 XX PR 28-JUN-2000; 2000US-0214886P.
 XX PR 30-JUN-2000; 2000US-0215135P.
 XX PR 07-JUL-2000; 2000US-0216647P.
 XX PR 07-JUL-2000; 2000US-0216880P.
 XX PR 11-JUL-2000; 2000US-0217487P.
 XX PR 11-JUL-2000; 2000US-0217496P.
 XX PR 14-JUL-2000; 2000US-0218290P.
 XX PR 26-JUL-2000; 2000US-0220933P.
 XX PR 26-JUL-2000; 2000US-0220933P.
 XX PR 14-AUG-2000; 2000US-0224518P.
 XX PR 14-AUG-2000; 2000US-0224519P.
 XX PR 14-AUG-2000; 2000US-0225213P.
 XX PR 14-AUG-2000; 2000US-0225214P.
 XX PR 14-AUG-2000; 2000US-0225215P.
 XX PR 14-AUG-2000; 2000US-0225267P.
 XX PR 14-AUG-2000; 2000US-022564P.
 XX PR 14-AUG-2000; 2000US-022568P.
 XX PR 14-AUG-2000; 2000US-022570P.
 XX PR 14-AUG-2000; 2000US-0225447P.
 XX PR 22-AUG-2000; 2000US-0225757P.
 XX PR 23-AUG-2000; 2000US-0225758P.
 XX PR 30-AUG-2000; 2000US-0225759P.
 XX PR 01-SEP-2000; 2000US-0226279P.
 XX PR 22-AUG-2000; 2000US-0226681P.
 XX PR 01-SEP-2000; 2000US-0226858P.
 XX PR 01-SEP-2000; 2000US-0227182P.
 XX PR 01-SEP-2000; 2000US-0229345P.
 XX PR 05-SEP-2000; 2000US-0229509P.
 XX PR 05-SEP-2000; 2000US-0229513P.
 XX PR 06-SEP-2000; 2000US-0230437P.
 XX PR 06-SEP-2000; 2000US-0230438P.
 XX PR 08-SEP-2000; 2000US-0231242P.
 XX PR 08-SEP-2000; 2000US-0231243P.
 XX PR 14-SEP-2000; 2000US-0231244P.
 XX PR 08-SEP-2000; 2000US-0231413P.
 XX PR 14-SEP-2000; 2000US-0231414P.
 XX PR 08-SEP-2000; 2000US-0232088P.
 XX PR 14-SEP-2000; 2000US-0232408P.
 XX PR 12-SEP-2000; 2000US-0231968P.
 XX PR 14-SEP-2000; 2000US-0232397P.
 XX PR 14-SEP-2000; 2000US-0232398P.
 XX PR 14-SEP-2000; 2000US-0232399P.
 XX PR 14-SEP-2000; 2000US-0233064P.
 XX PR 14-SEP-2000; 2000US-0233065P.
 XX PR 21-SEP-2000; 2000US-02334223P.
 XX PR 21-SEP-2000; 2000US-0234274P.
 XX PR 25-SEP-2000; 2000US-0234997P.
 XX PR 25-SEP-2000; 2000US-0234998P.
 XX PR 26-SEP-2000; 2000US-0235484P.
 XX PR 27-SEP-2000; 2000US-0235834P.
 XX PR 27-SEP-2000; 2000US-0235836P.
 XX PR 29-SEP-2000; 2000US-0236327P.
 XX PR 29-SEP-2000; 2000US-0236367P.
 XX PR 29-SEP-2000; 2000US-0236368P.
 XX PR 29-SEP-2000; 2000US-0236369P.
 XX PR 02-OCT-2000; 2000US-0236802P.
 XX PR 02-OCT-2000; 2000US-0237037P.
 XX PR 02-OCT-2000; 2000US-0237038P.
 XX PR 02-OCT-2000; 2000US-0237039P.
 XX PR 02-OCT-2000; 2000US-0237040P.
 XX PR 13-OCT-2000; 2000US-023935P.
 XX PR 13-OCT-2000; 2000US-023937P.
 XX PR 20-OCT-2000; 2000US-0241960P.
 XX PR 20-OCT-2000; 2000US-0241960P.
 XX PR 20-OCT-2000; 2000US-0241961P.
 XX PR 20-OCT-2000; 2000US-0241962P.
 XX PR 20-OCT-2000; 2000US-0241963P.
 XX PR 20-OCT-2000; 2000US-0241964P.
 XX PR 20-OCT-2000; 2000US-0241965P.
 XX PR 20-OCT-2000; 2000US-0241966P.
 XX PR 20-OCT-2000; 2000US-0241967P.
 XX PR 01-NOV-2000; 2000US-0241968P.
 XX PR 08-NOV-2000; 2000US-0241786P.
 XX PR 08-NOV-2000; 2000US-0241787P.
 XX PR 08-NOV-2000; 2000US-0241808P.
 XX PR 08-NOV-2000; 2000US-0241809P.
 XX PR 08-NOV-2000; 2000US-0241826P.
 XX PR 01-NOV-2000; 2000US-0241827P.
 XX PR 08-NOV-2000; 2000US-02418617P.
 XX PR 08-NOV-2000; 2000US-02418618P.
 XX PR 08-NOV-2000; 2000US-0246474P.
 XX PR 08-NOV-2000; 2000US-0246475P.
 XX PR 08-NOV-2000; 2000US-0246476P.
 XX PR 08-NOV-2000; 2000US-0246477P.
 XX PR 08-NOV-2000; 2000US-0246578P.
 XX PR 08-NOV-2000; 2000US-0246523P.
 XX PR 08-NOV-2000; 2000US-0246532P.
 XX PR 08-NOV-2000; 2000US-0246609P.
 XX PR 08-NOV-2000; 2000US-0246610P.
 XX PR 08-NOV-2000; 2000US-0246611P.
 XX PR 08-NOV-2000; 2000US-0246613P.
 XX PR 17-NOV-2000; 2000US-0246528P.
 XX PR 08-NOV-2000; 2000US-0246532P.
 XX PR 08-NOV-2000; 2000US-0246609P.
 XX PR 08-NOV-2000; 2000US-0246610P.
 XX PR 08-NOV-2000; 2000US-0246611P.
 XX PR 17-NOV-2000; 2000US-0246613P.
 XX PR 17-NOV-2000; 2000US-0246614P.
 XX PR 17-NOV-2000; 2000US-0246615P.
 XX PR 17-NOV-2000; 2000US-0246616P.
 XX PR 17-NOV-2000; 2000US-0246617P.
 XX PR 17-NOV-2000; 2000US-0246618P.
 XX PR 17-NOV-2000; 2000US-0246619P.
 XX PR 17-NOV-2000; 2000US-0246620P.
 XX PR 17-NOV-2000; 2000US-0246621P.
 XX PR 17-NOV-2000; 2000US-0246622P.
 XX PR 17-NOV-2000; 2000US-0246623P.
 XX PR 17-NOV-2000; 2000US-0246624P.
 XX PR 17-NOV-2000; 2000US-0246625P.
 XX PR 17-NOV-2000; 2000US-0246626P.
 XX PR 17-NOV-2000; 2000US-0246627P.
 XX PR 17-NOV-2000; 2000US-0246628P.
 XX PR 17-NOV-2000; 2000US-0246629P.
 XX PR 17-NOV-2000; 2000US-0246630P.
 XX PR 01-DEC-2000; 2000US-0250160P.
 XX PR 01-DEC-2000; 2000US-0250391P.
 XX PR 05-DEC-2000; 2000US-0251030P.
 XX PR 05-DEC-2000; 2000US-0251988P.
 XX PR 05-DEC-2000; 2000US-0256712P.
 XX PR 06-DEC-2000; 2000US-0251479P.
 XX PR 08-DEC-2000; 2000US-02518567P.
 XX PR 08-DEC-2000; 2000US-0251868P.

PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX DR 2001-483426/52.
 DR N-PSDB; AAK56533.
 XX PT Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 PS Claim 11; SEQ ID NO 11345; 3071pp + Sequence Listing; English.
 XX
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention
 XX Sequence 67 AA;

Query Match 25.0%; Score 5; DB 4; Length 67;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 36 PRGAP 40

Query Match 25.0%; Score 5; DB 4; Length 67;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 40 PRGAP 44

Query Match 25.0%; Score 5; DB 5; Length 67;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 40 PRGAP 44

RESULT 63
 ABP64418
 ID ABP64418 standard; protein; 67 AA.
 XX
 AC ABP64418;
 XX DT 04-NOV-2002 (First entry)
 DE Human ORF788.
 KW Cytostatic; Cardiant; Anti-allergic; Immunosuppressive; Vulnerary;
 KW Antinflammatory; gene therapy; human; OREX; atherogenic; Platelet;
 KW human umbilical vein endothelial cell; HUVEC; atherosclerotic plaque;
 KW cancer; cardiovascular disease; allergy; autoimmune disease;
 KW wound healing; blood coagulation disorder; inflammatory disorder.
 XX OS Homo sapiens.
 XX PN US2002082206-A1.
 XX PD 27-JUN-2002.
 XX PP 30-MAY-2001; 2001US-00867550.
 XX PR 30-MAY-2000; 2000US-0208427P.
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PA (LEACH/) LEACH M D.
 PA (MEHR/) MEHRABAN F.
 PA (CONLY/) CONLEY P B.
 PA (TOPP/) TOPPER J N.
 PA (LAWD/) LAW D.
 XX
 PI Leach MD, Mehraban F, Conley PB, Topper JN, Law D;
 XX DR WPI; 2002-626554/67.
 DR N-PSDB; AB098981.
 XX
 PT New polypeptide designated OREX are present in human atherogenic cells
 PT and are useful to prevent and treat OREX-associated disorders including
 PT cancer, allergy, wound healing or autoimmune, cardiovascular, or
 PT inflammatory disease.
 XX
 PS Claim 10; SEQ ID NO 1576; 78pp; English.
 XX
 CC The present invention relates to novel human OREX polypeptides and their
 CC coding sequences (ABP6361-ABP64681, and ABQ98194-ABQ9967). The sequences
 CC were discovered in human atherogenic cells, in particular in platelets
 CC and human umbilical vein endothelial cells (HUVEC) and are expressed in
 CC many other tissues as well. Atherogenic cells are cells which have the
 CC potential to develop atherosclerotic plaques. The OREX polypeptides and
 CC nucleic acids are useful for treating or preventing a pathological
 CC condition associated with an OREX-associated disorder, e.g. cancer,
 CC cardiovascular disease, allergy, autoimmune disease, wound healing, blood
 CC coagulation disorders or inflammatory disorders. Note: The sequence data
 CC obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/sequence.html?DocID=20020082206
 XX Sequence 67 AA;

Query Match 25.0%; Score 5; DB 5; Length 67;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 40 PRGAP 44

RESULT 64
 AAU61722 standard; protein; 68 AA.
 XX
 AC AAU61722;
 XX DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #22618.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatopathy; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX PN WO200181581-A2.
 XX PD 01-NOV-2001.
 XX PF 20-APR-2001; 2001W0-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-020841P.
 PR 07-JUL-2000; 2000US-0216747P.
 PA (CORT-) CORIXA CORP.
 XX
 PI

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX WPI; 2001-616774/71.
 DR N-PSDB; AAS59820.
 Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX Example 1; SEQ ID NO 22917; 106pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 68 AA;

Query Match	25.0%	Score 5;	DB 4;	Length 68;
Best Local Similarity	100.0%	Pred. No. 3.5e+02;		
Matches	5;	Conservative	0;	Mismatches 0;
Db	61	PRGAP	65	Indels 0;
Qy	1	PRGAP	5	Gaps 0;

XX RESULT 65
 ABM58241 standard; protein; 68 AA.
 XX AC
 XX DT 20-OCT-2003 (first entry)
 XX Propionibacterium acnes predicted ORF-encoded polypeptide #22917.
 DE XX
 KW Acne vulgaris; antiseborrhoeic; dermatological; antibacterial;
 KW immunostimulant; immune response; vaccine.
 XX OS Propionibacterium acnes.
 PN WO2003033515-A1.
 XX PR 11-OCT-2002; 2002WO-US032727.
 XX PR 15-OCT-2001; 2001US-00978825.
 PA (CORIXA) CORIXA CORP.
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Valliere-Douglas J;
 XX PR 2003-381789/36.

DR N-PSDB; ACF64549.
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
 XX Example 1; SEQ ID NO 22917; 1481pp; English.

CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624 ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition comprising P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide; a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 68 AA;

Query Match	25.0%	Score 5;	DB 6;	Length 68;
Best Local Similarity	100.0%	Pred. No. 3.5e+02;		
Matches	5;	Conservative	0;	Mismatches 0;
Db	61	PRGAP	65	Indels 0;
Qy	1	PRGAP	5	Gaps 0;

XX RESULT 66
 AAG57909 standard; protein; 70 AA.
 XX AC
 XX DT 18-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 74689.
 DE XX Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 XX OS Arabidopsis thaliana.
 PN EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PF 25-FEB-2000; 2000EP-00301439.
 XX PR 25-FEB-1999; 99US-0121835P.
 PR 05-MAR-1999; 99US-0123180P.
 PR 09-MAR-1999; 99US-0123548P.
 PR 23-MAR-1999; 99US-0125788P.

PR	25-MAR-1999;	99US-0126264P.	PR	16-JUL-1999;	99US-0144086P.
PR	29-MAR-1999;	99US-0126785P.	PR	19-JUL-1999;	99US-014432P.
PR	01-APR-1999;	99US-0127462P.	PR	19-JUL-1999;	99US-014431P.
PR	06-APR-1999;	99US-0128234P.	PR	19-JUL-1999;	99US-014432P.
PR	08-APR-1999;	99US-0128714P.	PR	19-JUL-1999;	99US-014433P.
PR	16-APR-1999;	99US-0129845P.	PR	19-JUL-1999;	99US-014433P.
PR	21-APR-1999;	99US-0130077P.	PR	19-JUL-1999;	99US-014433P.
PR	23-APR-1999;	99US-0130449P.	PR	20-JUL-1999;	99US-014435P.
PR	05-MAY-1999;	99US-0130510P.	PR	20-JUL-1999;	99US-014463P.
PR	28-APR-1999;	99US-0130891P.	PR	20-JUL-1999;	99US-0144834P.
PR	30-APR-1999;	99US-0131449P.	PR	21-JUL-1999;	99US-014483P.
PR	04-MAY-1999;	99US-0132048P.	PR	21-JUL-1999;	99US-0145086P.
PR	04-MAY-1999;	99US-0132407P.	PR	21-JUL-1999;	99US-0145088P.
PR	05-MAY-1999;	99US-0132484P.	PR	22-JUL-1999;	99US-0145088P.
PR	06-MAY-1999;	99US-0132486P.	PR	22-JUL-1999;	99US-0145099P.
PR	07-MAY-1999;	99US-0132487P.	PR	22-JUL-1999;	99US-0145122P.
PR	11-MAY-1999;	99US-0132863P.	PR	23-JUL-1999;	99US-014515P.
PR	14-MAY-1999;	99US-0133256P.	PR	23-JUL-1999;	99US-0145238P.
PR	14-MAY-1999;	99US-01334210P.	PR	23-JUL-1999;	99US-0145244P.
PR	14-MAY-1999;	99US-01334219P.	PR	22-JUL-1999;	99US-014526P.
PR	14-MAY-1999;	99US-01334221P.	PR	27-JUL-1999;	99US-0145943P.
PR	18-MAY-1999;	99US-01334370P.	PR	27-JUL-1999;	99US-014598P.
PR	20-MAY-1999;	99US-01334941P.	PR	28-JUL-1999;	99US-014591P.
PR	21-MAY-1999;	99US-01335353P.	PR	02-AUG-1999;	99US-0146366P.
PR	24-MAY-1999;	99US-01335629P.	PR	02-AUG-1999;	99US-0146388P.
PR	25-MAY-1999;	99US-01336021P.	PR	02-AUG-1999;	99US-014639P.
PR	27-MAY-1999;	99US-013392P.	PR	03-AUG-1999;	99US-0147038P.
PR	28-MAY-1999;	99US-01339540P.	PR	04-AUG-1999;	99US-0147204P.
PR	01-JUN-1999;	99US-01337222P.	PR	04-AUG-1999;	99US-0147302P.
PR	03-JUN-1999;	99US-0137528P.	PR	05-AUG-1999;	99US-0147192P.
PR	04-JUN-1999;	99US-0137502P.	PR	05-AUG-1999;	99US-0147260P.
PR	07-JUN-1999;	99US-0137724P.	PR	06-AUG-1999;	99US-0147303P.
PR	08-JUN-1999;	99US-0138094P.	PR	06-AUG-1999;	99US-0147416P.
PR	10-JUN-1999;	99US-0138540P.	PR	09-AUG-1999;	99US-0147933P.
PR	18-JUN-1999;	99US-0138847P.	PR	09-AUG-1999;	99US-0147945P.
PR	14-JUN-1999;	99US-0139119P.	PR	10-AUG-1999;	99US-0148119P.
PR	16-JUN-1999;	99US-013945P.	PR	11-AUG-1999;	99US-014760P.
PR	16-JUN-1999;	99US-0139453P.	PR	12-AUG-1999;	99US-0148341P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-014856P.
PR	18-JUN-1999;	99US-0139454P.	PR	13-AUG-1999;	99US-014884P.
PR	18-JUN-1999;	99US-0139450P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149219P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-014922P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139459P.	PR	23-AUG-1999;	99US-014992P.
PR	01-JUL-1999;	99US-0139460P.	PR	27-AUG-1999;	99US-014992P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-0150566P.
PR	23-JUN-1999;	99US-014054P.	PR	31-AUG-1999;	99US-0151438P.
PR	24-JUN-1999;	99US-0139750P.	PR	01-SEP-1999;	99US-0151930P.
PR	28-JUN-1999;	99US-014055P.	PR	07-SEP-1999;	99US-0152363P.
PR	29-JUN-1999;	99US-0140563P.	PR	10-SEP-1999;	99US-015106P.
PR	30-JUN-1999;	99US-0140591P.	PR	13-SEP-1999;	99US-0153070P.
PR	22-JUN-1999;	99US-014287P.	PR	15-SEP-1999;	99US-0153758P.
PR	01-JUL-1999;	99US-0143999P.	PR	30-AUG-1999;	99US-0155659P.
PR	01-JUL-1999;	99US-0144842P.	PR	16-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0140695P.	PR	22-SEP-1999;	99US-015139P.
PR	06-JUL-1999;	99US-0142055P.	PR	23-SEP-1999;	99US-0152486P.
PR	08-JUL-1999;	99US-0142390P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142203P.	PR	28-SEP-1999;	99US-015645BP.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-015659P.
PR	13-JUL-1999;	99US-0143542P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0144624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.

PR 08-OCT-1999; 990US-0158232P.
 PR 12-OCT-1999; 990US-0158369P.
 PR 13-OCT-1999; 990US-0158329P.
 PR 13-OCT-1999; 990US-0158294P.
 PR 13-OCT-1999; 990US-0158295P.
 PR 14-OCT-1999; 990US-0158329P.
 PR 14-OCT-1999; 990US-0158330P.
 PR 14-OCT-1999; 990US-0158331P.
 PR 14-OCT-1999; 990US-0158332P.
 PR 14-OCT-1999; 990US-0158637P.
 PR 14-OCT-1999; 990US-0158638P.
 PR 18-OCT-1999; 990US-0159844P.
 PR 21-OCT-1999; 990US-0160741P.
 PR 21-OCT-1999; 990US-0160767P.
 PR 21-OCT-1999; 990US-0160768P.
 PR 21-OCT-1999; 990US-0160770P.
 PR 21-OCT-1999; 990US-0160814P.
 PR 21-OCT-1999; 990US-0160815P.
 PR 22-OCT-1999; 990US-0160980P.
 PR 22-OCT-1999; 990US-016081P.
 PR 22-OCT-1999; 990US-016081P.
 PR 25-OCT-1999; 990US-016089P.
 PR 25-OCT-1999; 990US-0161404P.
 PR 25-OCT-1999; 990US-0161405P.
 PR 26-OCT-1999; 990US-0161359P.
 PR 26-OCT-1999; 990US-0161360P.
 PR 28-OCT-1999; 990US-0161361P.
 PR 28-OCT-1999; 990US-0161202P.
 PR 28-OCT-1999; 990US-0161992P.
 PR 28-OCT-1999; 990US-0161933P.
 PR 29-OCT-1999; 990US-0162142P.
 PR 29-OCT-1999; 990US-0162142P.

Query Match Score 5; DB 3; Length 70;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 63 OMLET 67

Query Match Score 5; DB 3; Length 70;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 63 OMLET 67

RESULT 67
 AAO10516 Human polypeptide SEQ ID NO 24408.
 ID AAO10516 standard; protein; 70 AA.
 AC AAO10516;
 XX 06-NOV-2001 (first entry)
 XX DE Human cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX OS Homo sapiens.
 XX PN WO200164835-A2.
 XX PD 07-SEP-2001.
 XX PR 26-FEB-2001; 2001WO-US004927.
 XX PR 28-FEB-2000; 2000US-0051516.
 XX PR 18-MAY-2000; 2000US-00577499.
 PA (HYSEQ-) HYSEQ INC.
 XX PI Tang YT, Liu C, Drmanac RT;
 XX DR WPI: 2001-514838/56.
 DR N-PsDB; AAI90447.

XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
 PT PT and treating e.g. leukemia, inflammation and immune disorders.
 XX XX
 PS Claim 20; SEQ ID NO 24408; 1399PP + Sequence Listing; English.
 CC The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA00010-AA013910) that exhibit activity relating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 Sequence 70 AA;
 SQ |||||
 Query Match Score 5; DB 4; Length 70;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 68
 AAU64459 standard; protein; 71 AA.
 ID AAU64459
 AC AAU64459;
 XX 27-FEB-2002 (first entry)
 XX DE Propionibacterium acnes immunogenic protein #25355.
 XX Propionibacterium acnes
 XX DE Propionibacterium acnes immunogenic protein #25355.
 XX XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX OS Propionibacterium acnes
 XX XX WO200181581-A2.
 XX PN 01-NOV-2001.
 XX PD 27-FEB-2002.
 XX PR 20-APR-2001; 2001WO-US012865.
 XX KW 01-NOV-2001.
 XX PR 21-APR-2000; 2000US-0199047P.
 XX PR 02-JUN-2000; 2000US-0208841P.
 XX PR 07-JUL-2000; 2000US-0216747P.
 XX XX (CORI-) CORIXA CORP.
 XX Skeik YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 XX DR WPI: 2001-616774/71.
 XX DR N-PsDB; AAS9644.
 PT Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
 PT Example 1; SEQ ID NO 25654; 1069PP; English.
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in
 CC CC

the treatment, prevention and diagnosis of medical conditions caused by *P. acnes*. The disorders include SAPHO syndrome (*synovitis, acne, pustulosis, hyperostosis and osteomyelitis*), uveitis and endophthalmitis. *P. acnes* is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of *P. acnes* in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

Sequence 71 AA;
Query Match 25.0%; Score 5; DB 4; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
DB 62 PRGAP 66

RESULT 69
ABM61978 standard; protein; 71 AA.
XX
AC ABM60378
ID ABM60378
XX
DT 20-OCT-2003 (First entry)
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25654.
XX
KW Acne vulgaris; antiseborhoeic; dermatological; antibacterial;
KW immunostimulant; immune response; vaccine.
XX
OS Propionibacterium acnes.
XX
PN WO2003033515-A1.
XX
PD 24-APR-2003.
XX
PP 11-OCT-2002; 2002WO-US032727.
XX
PR 15-OCT-2001; 2001US-00978825.
XX
(CORY-) CORIXA CORP.

PI Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Carter D;
PI Barth B, Valliere-Douglas J;
XX
DR WPI; 2003-381789/36.
N-PSDB; ACF64573.
XX
PR New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a *P. acnes* protein.

XX
PS Example 1; SEQ ID NO 25654; 1481pp; English.
XX
The invention relates to an isolated polynucleotide (ACF64435-ACF64733) encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of *P. acnes* polypeptides. The invention additionally encompasses expression vectors and host cells comprising a

CC polynucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a *P. acnes* polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising *P. acnes* polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of *P. acnes* in a patient; and a method for inhibiting the development of *P. acnes* in a patient. The *P. acnes* polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a *P. acnes* protein. The polynucleotides can also be used as probes or primers for stimulation of an immune response against *P. acnes*, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the *P. acnes* polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

SQ Sequence 71 AA;
Query Match 25.0%; Score 5; DB 6; Length 71;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
RESULT 70
ABM14327
ID AAM14327 standard; protein; 72 AA.
XX
AC AAM14327;
XX
DT 12-OCT-2001 (first entry)
XX
Peptide #761 encoded by probe for measuring cervical gene expression.
DE Probe; human; microarray; gene expression; cervical epithelial cell;
XX
RN cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US006070.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632356.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000US-00024263.
XX
(MOLE-) MOLECULAR DYNAMICS INC.
XX
Penn SG, Hanzel DK, Chen W, Rank DR;
XX
WPI; 2001-488901/53.

XX
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
XX
Claim 27; SEQ ID NO 19153; 487pp; English.
PS

The present invention relates to human single exon nucleic acid probes (SENPs; see AAU0068-AAU2859). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <http://www.wipo.int/pctdb/patent/pct.html>.

X Sequence 72 AA;

RESULT 71

XX	ABCB3	Standard 1;
AC	ABB33274;	
AT	04-FEB-2002	(first entry)
XX	Peptide #780 encoded by human foetal liver single exon probe.	
XX	Human; foetal liver; gene expression; single exon nucleic acid probe.	
XX		Homo sapiens.
DS		

PN WO200157277-A2.

PD	09-AUG-2001.	2001WO-US000669.
XXX	30-JAN-2001;	2001WO-US000669.
PPF	04-FEB-2000;	2000US-0180312P.
XXX	26-MAY-2000;	2000US-0207456P.
PPR	30-JUN-2000;	2000US-0060840B.
PPR	03-AUG-2000;	2000US-00632366.
PPR	21-SEP-2000;	2000US-0234687P.
PPR	27-SEP-2000;	2000US-02346359P.
PPR	04-OCT-2000;	2000US-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX

DR WPI; 2001-483447/52.
XXX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.
XX Claim 27: SEQ ID NO 25909; 639pp + Sequence Listing; English.
XX CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in sample derived from human fetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
CC
XX Sequence 72 AA:
XX SO
XX

```

Query Match      25.0%; Score 5; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 PRGAP 5
Db      16 PRGAP 20

RESULT 72
AAM26737 standard; protein; 72 AA.
ID AAM26737
XX
AC
XX
XX
DT 17-OCT-2001 (first entry)
XX Peptide #774 encoded by probe for measuring placental gene expression.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO2001572-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-018012P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0234659P.
PR 04-OCT-2000; 2000US-02346263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 27006; 654PP; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENPs);
CC see AAI31315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 72 AA;

Query Match      25.0%; Score 5; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      1 PRGAP 5
Db      16 PRGAP 20

RESULT 73
ABB28100
ID ABB28100 standard; peptide; 72 AA.
XX
AC
XX

```

DT 01-FEB-2002 (first entry)
 XX Human Peptide #751 encoded by breast cell single exon nucleic acid probe.
 DE XX Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer.
 XX OS Homo sapiens.
 XX PN WO200157271-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US000662.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207416P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234617P.
 PR 27-SEP-2000; 2000US-0234687P.
 PR 04-OCT-2000; 2000US-0236339P.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2001-49693/54.
 XX PT New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX PS Claim 27; SEQ ID NO 11068; 322pp + Sequence Listing; English.
 XX CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosis of breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC gene expression, with far greater diversity of probes for measuring
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp://wipo.int/pub/published_pct_sequences
 XX SQ Sequence 72 AA;
 CC Query Match 25.0%; Score 5; DB 4; Length 72;
 CC Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC AC AAM66456;
 CC XX DT 06-NOV-2001 (first entry)
 CC DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26762.
 CC XX ID AAM66456 standard; protein; 72 AA.
 CC KW Human; bone marrow expressed exon; gene expression analysis; probe;
 CC AC Homo sapiens.
 CC XX PN WO200157276-A2.

RESULT 74
 ABB18736
 ID ABB18736 standard; protein; 72 AA.
 XX AC ABB18736;
 DT 23-JAN-2002 (first entry)
 XX

RESULT 75
 AAM66456
 ID AAM66456 standard; protein; 72 AA.
 XX AC AAM66456;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26762.
 XX ID AAM66456 standard; protein; 72 AA.
 XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
 XX AC Homo sapiens.
 XX PN WO200157276-A2.

XX
 PD 09-AUG-2001.
 XX
 PP 30-JAN-2001; 2001W0-US000668.
 XX
 PR 04-FEB-2000; 2000US-0160312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-0207456P.
 PR 2000US-00508408.
 PR 03-AUG-2000; 2000US-00508408.
 PR 21-SEP-2000; 2000US-00532366.
 PR 27-SEP-2000; 2000US-0234687P.
 PR 04-OCT-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488900/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX
 PS Example 4; SEQ ID NO 26762; 658pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX
 SQ Sequence 72 AA;
 Query Match Score 5; DB 4; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 |||||
 Db 16 PRGAP 20

Search completed: October 26, 2004, 07:16:20
 Job time : 92 secs

Result No.	Score	Query Match Length DB ID	Description
1	20	100.0 20 14 US-10-066-965A-3	Sequence 3, Appli
2	20	100.0 20 14 US-10-066-965A-22	Sequence 22, Appli
3	7	35.0 20 14 US-10-066-965A-4	Sequence 4, Appli
4	7	35.0 14 US-10-066-965A-23	Sequence 23, Appli
5	6	30.0 34 15 US-10-066-965A-4	Sequence 341, Appli
6	6	30.0 253 16 US-10-0437-963-114356	Sequence 114356, Appli
7	6	30.0 262 15 US-10-4314-67611	Sequence 67611, Appli
8	6	30.0 324 16 US-10-479-334-26	Sequence 26, Appli
9	6	30.0 731 16 US-10-408-765A-2869	Sequence 2869, Appli
10	5	25.0 9 9 US-09-834-765-634	Sequence 528, Appli
11	5	25.0 9 9 US-09-834-765-583	Sequence 634, Appli
12	5	25.0 10 9 US-09-834-765-583	Sequence 583, Appli
13	5	25.0 20 14 US-10-280-066-66	Sequence 66, Appli

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB ID	Description
1	20	100.0 20 14 US-10-066-965A-3	Sequence 3, Appli
2	20	100.0 20 14 US-10-066-965A-22	Sequence 22, Appli
3	7	35.0 20 14 US-10-066-965A-4	Sequence 4, Appli
4	7	35.0 14 US-10-066-965A-23	Sequence 23, Appli
5	6	30.0 34 15 US-10-066-965A-4	Sequence 341, Appli
6	6	30.0 253 16 US-10-0437-963-114356	Sequence 114356, Appli
7	6	30.0 262 15 US-10-4314-67611	Sequence 67611, Appli
8	6	30.0 324 16 US-10-479-334-26	Sequence 26, Appli
9	6	30.0 731 16 US-10-408-765A-2869	Sequence 2869, Appli
10	5	25.0 9 9 US-09-834-765-634	Sequence 528, Appli
11	5	25.0 9 9 US-09-834-765-583	Sequence 634, Appli
12	5	25.0 10 9 US-09-834-765-583	Sequence 583, Appli
13	5	25.0 20 14 US-10-280-066-66	Sequence 66, Appli

Sequence 25, Appli

RESULT 1
US-10-066-965A-3
; Sequence 3, Application US/10066965A
; Publication No. US20030143626A1
; GENERAL INFORMATION:
; APPLICANT: COHEN, BARAK A.
; APPLICANT: BRENT, ROGER
; APPLICANT: COLAS, PIERRE
; TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
; FILE REFERENCE: EGYP 3.0-015
; CURRENT APPLICATION NUMBER: US/10/066, 965A
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-066-965A-3

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e-15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAPMMRWVQMLETMFL 20
Db 1 PRGAPMMRWVQMLETMFL 20

RESULT 2
US-10-066-965A-22
; Sequence 22, Application US/10066965A
; Publication No. US20030143626A1
; GENERAL INFORMATION:
; APPLICANT: BRENT, ROGER
; APPLICANT: COHEN, BARAK A.
; APPLICANT: COLAS, PIERRE
; TITLE OF INVENTION: TARGETED MODIFICATION OF INTRACELLULAR COMPOUNDS
; FILE REFERENCE: EGYP 3.0-015
; CURRENT APPLICATION NUMBER: US/10/066, 965A
; CURRENT FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-066-965A-22

Query Match 100.0%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAPMW 7
Db 1 PRGAPMW 7

RESULT 5
US-10-264-049-4341
; Sequence 4341, Application US/10264049
; Publication No. US2004005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAI3P1
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4341
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-049-4341
Query Match 30.0%; Score 6; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 LETMFL 20
Db 2 LETMFL 7

RESULT 6
US-10-437-963-114356
; sequence 114356, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 3B-21(53221)B
; CURRENT FILING NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114356
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18055C.1.pep

Query Match 30.0%; Score 6; DB 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
US-10-445-114-67611
; Sequence 67611, Application US/10425114
; Publication No. US2004034888A1
; GENERAL INFORMATION:

Qy 3 GAPMM 8
Db 18 GAPMM 23

RESULT 8
US-10-479-334-26
; Sequence 26, Application US/10479334
; Publication No. US2004013744A1
; GENERAL INFORMATION:
; APPLICANT: KAMANAKA, Shinya
; APPLICANT: KAIHO, Hideko
; TITLE OF INVENTION: GENES WITH ES CELL-SPECIFIC EXPRESSION
; FILE REFERENCE: 225475
; CURRENT APPLICATION NUMBER: US/10/479,334
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: PCT/JP02/05350
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: JP 2001-165927
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-479-334-26

Query Match 30.0%; Score 6; DB 16; Length 324;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMFL 20
Db 210 LETMFL 215

RESULT 9
US-10-408-765A-2869
; Sequence 2869, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fathy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.

RESULT 10
US-09-834-765-528
Sequence 528, Application US/09834765
GENERAL INFORMATION:
Patent No. US20020105478A1
APPLICANT: Mary Paris
APPLICANT: Pia M. Challita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
FILE REFERENCE: 129.676S1
CURRENT APPLICATION NUMBER: US/09/834-765
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 528
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-066-965a-3
CURRENT FILING DATE: 2003-04-04
SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 2869
LENGTH: 731
TYPE: PRT
ORGANISM: Homo sapiens
US-10-08-765a-2869
Query Match Score 6; DB 16; Length 731;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAPM 6
Db 542 PRGAPM 542

RESULT 12
US-09-834-765-583
Sequence 583, Application US/09834765
GENERAL INFORMATION:
Patent No. US20020105478A1
APPLICANT: Mary Paris
APPLICANT: Pia M. Challita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
FILE REFERENCE: 129.676S1
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 583
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-765-583

RESULT 13
US-10-280-066-66
Sequence 66, Application US/10280066
GENERAL INFORMATION:
Publication No. US20030180718A1
APPLICANT: Pillatia, Renuka C.
APPLICANT: Brissette, Renee
APPLICANT: Sprout, Michael
APPLICANT: Dedorva, Olga
APPLICANT: Blume, Arthur J.
APPLICANT: Prendergast, John
APPLICANT: Goldstein, Neil I.
TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINDING
FILE REFERENCE: 2558-4009US1
CURRENT APPLICATION NUMBER: US/10/280,066
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 60/345,471
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 537

SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 66
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGI-2-20R-4-G114
; US-10-280-066-66

Query Match 25.0%; Score 5; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MNMRW 10
Db 8 MNMRW 12

RESULT 14
US-10-231-417-416
; Sequence 416, Application US/10231417
; Publication No. US20030176681A1
; GENERAL INFORMATION:
; APPLICANT: Peng et al.
; TITLE OF INVENTION: 148 Human Secreted Proteins
; FILE REFERENCE: PZ019P1
; CURRENT APPLICATION NUMBER: US/10/2331,417
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US/09/296,622
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 619
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 416
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-231-417-416

Query Match 25.0%; Score 5; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 QMML 16
Db 3 QMML 7

RESULT 15
US-10-437-963-120828
; Sequence 120828, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Title of Invention: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 120828
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23912C.1.pep

Query Match 25.0%; Score 5; DB 16; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VCQML 15
Db 10 VCQML 14

RESULT 16
US-09-864-761-35124
; Sequence 35124, Application US/09864761
; GENERAL INFORMATION:
; PATENT NO. US20040148763A1
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 35124
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007688.15
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1

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; OTHER INFORMATION: EXPRESSED IN HEMLA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.99
; OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EST_HUMAN HIT: R77154.1, EVALUUE 1.00e-08
US-09-864-761-35124

Query Match Score 5; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGAPM 6
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Db 20 RGAPM 24
      ||||

RESULT 17
US-09-864-761-45993
; Sequence 45993, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;   APPLICANT: Penn, Sharron G.
;   APPLICANT: Rank, David R.
;   APPLICANT: Hanzel, David K.
;   APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Amnonax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 45993
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; OTHER INFORMATION: MAP TO AC005323.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2e+02
; OTHER INFORMATION: EST_HUMAN HIT: BF33300.1, EVALUUE 4.00e+00
US-09-864-761-45993

Query Match Score 5; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QMLET 17
      |||||
Db 32 QMLET 36
      |||||
```

RESULT 18

US-10-815-514-6

; Sequence 6, Application US/10815514
; Publication No. US20040204161A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Maynew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/85,514
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US/09/696,872
; PRIOR FILING DATE: 2000-11-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-815-514-6

Query Match Score 5; DB 17; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETMFL 20
 |||||
Db 31 ETMFL 35
 |||||

RESULT 19

US-09-864-761-38656

; Sequence 38656, Application US/09B64761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David R.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Amnonax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 45993
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens

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; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-10
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 3864-761-38656
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006024.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EST HUMAN HIT: BF241410.1, EVALUE 6.00e-01
; LENGTH: 47
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 204604
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Cryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_99675C.1.pep
; US-10-437-963-204604

Query Match 25.0%; Score 5; DB 16; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 44 PRGAP 48

RESULT 21
US-10-424-599-267231
; Sequence 267231, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; NUMBER OF SEQ ID NOS: 49117
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285664
; SEQ ID NO: 267231
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8332C.1.pep
; US-10-424-599-267231

Query Match 25.0%; Score 5; DB 15; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VCOML 15
Db 41 VCOML 45

RESULT 22
US-10-152-031-13
; Sequence 13, Application US/10152031
; Publication No. US2003044825A1
; GENERAL INFORMATION:
; APPLICANT: IMAI, Yuji
; APPLICANT: AKATSUKA, Hiroyuki
; APPLICANT: OMORI, Eri
; APPLICANT: OMORI, Kenji
; APPLICANT: YANAKA, No. US20030044825A1
; APPLICANT: SAKURAI, Naoki
; TITLE OF INVENTION: Bone Metabolism Related Protein and Gene Thereof
; FILE REFERENCE: 0283-0163P
; CURRENT APPLICATION NUMBER: US/10/152,031
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,318
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: JP 318226/1998
; PRIOR FILING DATE: 2000-05-23
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 13
; LENGTH: 54

Query Match 25.0%; Score 5; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 13 PRGAP 17

RESULT 20
US-10-437-963-204604
; Sequence 204604, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; NUMBER OF SEQ ID NOS: 16
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; CURRENT FILING DATE: 2003-05-14

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TYPE: PRT ; ORGANISM: Mus musculus
US-10-152-031-13

Query Match 23 ; Best Local Similarity 100.0%; Score 5; DB 14; Length 54;
Matches 5; Conservative 0; Pred. No. 2.7e+02; Indels 0; Gaps 0;
Qy 2 RGAPM 6
Db 4 RGAPM 8

RESULT 24 ; Sequence 262093, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

Query Match 25.0%; Score 5; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 13 PRGAP 17

RESULT 25 ; Sequence 219441, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

Query Match 25.0%; Score 5; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 14 MLETM 18
Db 9 MLETM 13

RESULT 26 ; Sequence 264712, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

Query Match 25.0%; Score 5; DB 15; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 LETMF 19
Db 17 LETMF 21

RESULT 27 ; Sequence 32143, Application US/10029386
US-10-059-386-32143
Query Match 25.0%; Score 5; DB 9; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029-386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 32143
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO 298883 .3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: SWISSPROT HIT: O43451, EVALUE 2.00e-03

Query Match
Best Local Similarity 25.0%; Score 5; DB 14; Length 63;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 15 ERGAP 19

RESULT 28
US-10-424-599-152702
; Sequence 152702, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424-599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 152702
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_108914C.1.pep

Query Match
Best Local Similarity 25.0%; Score 5; DB 15; Length 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MMWRW 10
Db 28 MMWRW 32

RESULT 29
US-10-424-599-225320
; Sequence 225320, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

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; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 150750
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) .. (68)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_107151C.1.pep
US-10-424-599-150750

Query Match Score 5; DB 15; Length 68;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MLETM 18
Db 21 MLETM 25

RESULT 32
US-09-864-761-34034
; Sequence 34034, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/10/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-09-774,203

RESULT 33
US-10-001-879-175
; Sequence 175, Application US/10001879
; Publication No. US2002127237A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferkey, Robert
; APPLICANT: Ali, Shujath
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
; FILE REFERENCE: DEX-0281
; CURRENT APPLICATION NUMBER: US/10/001,879
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,188
; PRIOR FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 201
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 175
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-879-175

Query Match Score 5; DB 9; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGAP 5
Db 16 PRGAP 20

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RESULT 34
US-10-437-963-102863
; Sequence 102863, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

```

RESULT 35
US-10-437-963-135152
; Sequence 135152, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 102863
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100348C.1.pep
US-10-437-963-102863

Query Match 25.0%; Score 5; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGAP 5
Db 30 PRGAP 34

RESULT 37
US-10-424-599-144203
; Sequence 144203, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 149863
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_101228C.1.pep
US-10-424-599-144203

Query Match 25.0%; Score 5; DB 15; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRGAP 5
Db 43 PRGAP 47

RESULT 38
US-10-424-599-149863
; Sequence 149863, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 149863
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106348C.1.pep
US-10-424-599-149863

Query Match 25.0%; Score 5; DB 15; Length 79;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 QMLET 17
Db 20 QMLET 24

RESULT 39
US-09-922-261-464
; Sequence 464, Application US/09922261
; Patent No. US2002011471A1
; GENERAL INFORMATION:
; APPLICANT: COGNENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stewart D.
; APPLICANT: Puranam, Kasuri
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999

RESULT 36
US-10-424-599-144203
; Sequence 144203, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.

PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006658
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006653
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006652
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006651
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006650
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006649
 PRIOR FILING DATE: 2001-01-21
 PRIOR APPLICATION NUMBER: US 50/234,687
 SOFTWARE: AnnoMAX Sequence Listing Engine vers. 1.1
 SEQ ID NO: 47995
 LENGTH: 96
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AB023057.1
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.66
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.67
 OTHER INFORMATION: EXPRESSED IN HUMAN HIT: B8B88511.1, EVALUE 1.00e-10
 US-09-864-761-47995

Query Match 25.0%; Score 5; DB 9; Length 86;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 30 PRGAP 34

RESULT 46
 US-10-424-599-180086
 ; Publication No. US20040331072A1
 GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovacic, David K
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5323) B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO: 180086
 LENGTH: 87
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_133632C.1.pep
 US-10-424-599-180086

Query Match 25.0%; Score 5; DB 15; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PMWNR 9
 Db 17 PMWNR 21

RESULT 47
 US-10-424-599-281783
 ; Sequence 281783, Application US/10424599
 ; Publication No. US20040331072A1
 GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovacic, David K
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53223) B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO: 281783
 LENGTH: 87
 TYPE: PRT
 ORGANISM: Glycine max
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT3847_96470C.1.pep
 US-10-424-599-281783

Query Match 25.0%; Score 5; DB 15; Length 87;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 61 PRGAP 65

RESULT 48
 US-10-437-963-102687
 ; Sequence 102687, Application US/10437963
 ; Publication No. US2004123343A1
 GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazarov, Brad
 ; APPLICANT: Li, Ping
 ; APPLICANT: Borkar, Brind
 ; APPLICANT: Title of Invention: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(53221) B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO: 102687
 ; LENGTH: 88
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_100186C.1.pep
 ; SEQ ID NO: 102687

Query Match 25.0%; Score 5; DB 16; Length 88;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 71 PRGAP 75

RESULT 49
 US-10-767-701-50033
 ; Sequence 50033, Application US/10767701
 ; Publication No. US20040172684A1
 ; GENERAL INFORMATION:

RESULT 50
US-10-437-963-127248
; Sequence 127248, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 127248
; LENGTH: 89
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3478-035-P1-K1-H10.pep

Query Match 25.0%; Score 5; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 11 VQOML 15
Db 53 VQOML 57

RESULT 50
US-10-437-963-127248
; Sequence 127248, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 127248
; LENGTH: 89
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2971BC.1.pep

Query Match 25.0%; Score 5; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 81 PRGAP 85

RESULT 51
US-10-437-963-115372
; Sequence 115372, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.

Query Match 25.0%; Score 5; DB 16; Length 92;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 35 PRGAP 39

RESULT 52
US-10-437-963-124347
; Sequence 124347, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 124347
; LENGTH: 92
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27095C.1.pep

Query Match 25.0%; Score 5; DB 16; Length 92;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 36 PRGAP 40

RESULT 53
US-10-437-963-115372
; Sequence 115372, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 115372
; LENGTH: 92
; TYPE: PRT
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18976C.1.pep
; US-10-437-963-115372

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; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO: 285684
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_38003C.1.pep
; US-10-424-599-217028

Qy 15 LETMF 19
Db 54 LETMF 58

RESULT 54
US-09-864-408A-7168
Sequence 7168. Application US/09864408A
Publication No. US20040009474A1
GENERAL INFORMATION:
APPLICANT: Leach, Martin D.
TITLE OF INVENTION: Human Polynucleotides and Polypeptides Encoded by Genes
FILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/206,690
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 7168
LENGTH: 94
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc feature
LOCATION: (1)-(1)
OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-7168

Query Match 25.0%; Score 5; DB 11; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 69 PRGAP 73

RESULT 55
US-10-437-963-153530
Sequence 153530. Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukhacov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966

Qy 1 PRGAP 5
Db 42 PRGAP 46

RESULT 56
US-10-767-701-47642
Sequence 47642. Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO: 47642
LENGTH: 95
TYPE: PRT
ORGANISM: Plants and Uses Thereof For Plant Improvement
FEATURE: OTHER INFORMATION: Plants and Uses Thereof For Plant Improvement
NAME/KEY: unsure
LOCATION: (1)-(95)
FEATURE: OTHER INFORMATION: unsure at all Xaa locations
NAME/KEY: unsure
LOCATION: (1)-(95)
FEATURE: OTHER INFORMATION: unsure at all Xaa locations
US-10-767-701-47642

Query Match 25.0%; Score 5; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 4.e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 42 PRGAP 46

RESULT 57
US-09-905-243-15
Sequence 15. Application US/09905243
Patent No. US2004062009A1
GENERAL INFORMATION:
APPLICANT: Taylor, Alexander H.
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
Immunoactivity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ For Windows Version 3.0
SEQ ID NO: 15
LENGTH: 96
TYPE: PRT
ORGANISM: Pan troglodytes
FEATURE: DOMAIN
NAME/KEY: DOMAIN

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Query Match 25.0%; Score 5; DB 9; Length 96;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 WVCQM 14
 Db 36 WVCQM 40

RESULT 60
 US-10-424-599-159333
; Sequence 159333, Application US/10424599
; General Information:
; Publication No. US20040031072A1
; General Information:
; Applicant: La Rosa, Thomas J.
; Applicant: Kovacic, David K.
; Applicant: Zhou, Yihua
; Applicant: Cao, Yongwei
; Title of Invention: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; Current Application Number: US/10/424,599
; Current Filing Date: 2003-04-28
; Number of SEQ ID NOS: 285684
; SEQ ID NO 142846
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114899C.1.pep

Query Match 25.0%; Score 5; DB 15; Length 97;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VCQML 15
 Db 90 VCQML 94

RESULT 61
 US-10-437-963-134702
; Sequence 134702, Application US/10437963
; General Information:
; Publication No. US20040123334A1
; General Information:
; Applicant: La Rosa, Thomas J.
; Applicant: Kovacic, David K.
; Applicant: Zhou, Yihua
; Applicant: Cao, Yongwei
; Applicant: Wu, Wei
; Applicant: Boukharov, Andrey A.
; Applicant: Barbazuk, Brad
; Title of Invention: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
; Current Application Number: US/10/437,963
; Current Filing Date: 2003-05-14
; Number of SEQ ID NOS: 204966
; SEQ ID NO 157410
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3644C.1.pep

Query Match 25.0%; Score 5; DB 16; Length 97;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 40 PRGAP 44

RESULT 62
US-10-156-761-8165
Sequence 8165, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8165
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-8165

Query Match 25.0%; Score 5; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETM 18
Db 1 MLETM 5

RESULT 63
US-10-424-599-155904
Sequence 155904, Application US/10424599
Publication No. US2004031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovacic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 155904
LENGTH: 98
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_111801C.1.pep
US-10-424-599-155904

Query Match 25.0%; Score 5; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VCOML 15
Db 2 VCOML 6

RESULT 64
US-09-986-480-303
Sequence 303, Application US/09886480
Publication No. US2003002799A1
GENERAL INFORMATION:
APPLICANT: Roser et al.
FILE REFERENCE: PS500P1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/134,068
PRIOR FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 456
SEQ ID NO 303
SEQ ID NO 303
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-09-986-480-303

Query Match 25.0%; Score 5; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 63 PRGAP 67

RESULT 65
US-10-437-963-104856
Sequence 104856, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Li, Ping
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbizuk, Brad
APPLICANT: Li, Ping
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbizuk, Brad
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104856
LENGTH: 100
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_10214C.1.pep
US-10-437-963-104856

Query Match 25.0%; Score 5; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 69 PRGAP 73

RESULT 66
US-10-424-599-267655
Sequence 267655, Application US/10424599
Publication No. US2004031072A1
GENERAL INFORMATION:

```

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 267655
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_833715C.1.pep
US-10-424-599-267655

Query Match 25.0%; Score 5; DB 15; Length 101;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Clone ID: PAT_MRT4530_82553C.1.pep
US-10-437-963-185681

Qy 12 COMLE 16
Db 89 COMLE 93

RESULT 67
US-10-264-237-1456
; Sequence 1456, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Burse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO: 1456
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (64)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1456

Query Match 25.0%; Score 5; DB 15; Length 103;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OTHER INFORMATION: Clone ID: PAT_MRT4530_84537C.1.pep
US-10-437-963-187877

Qy 11 VCQML 15
Db 25 VCQML 29

RESULT 68
US-10-437-963-185681
; Sequence 185681, Application US/10437963
; Publication No. US20040123343A1

```

```

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204956
; SEQ ID NO: 195845
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE: NAME/KEY: unsure
; LOCATION: (1)..(103)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT4530_91754C.1.pep
; US-10-437-963-195845

Query Match Score 5; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 77 PRGAP 81
RESULT 71
US-10-767-701-60687
; Sequence 60687, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO: 60687
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE: OTHER INFORMATION: Clone ID: 9281056.pep
; US-10-767-701-60687

Query Match Score 5; DB 16; Length 103;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RGAPM 6
Db 91 RGAPM 95
RESULT 72
US-10-425-114-46232
; Sequence 46232, Application US/10425114
; Publication No. US2004034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovacic, David K.
; APPLICANT: Cao, Jack E.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO: 46232
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: 701130375_FLI.pep
; US-10-425-114-46232

Query Match Score 5; DB 15; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 LETMF 19
Db 79 LETMF 83
RESULT 73
US-10-424-599-216376
; Sequence 216376, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 216376
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: NAME/KEY: unsure
; LOCATION: (1)..(105)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_37416C.1.pep
; US-10-424-599-216376

Query Match Score 5; DB 15; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RGAPM 6
Db 73 RGAPM 77
RESULT 74
US-10-437-963-126718
; Sequence 126718, Application US/10437963
; Publication No. US2004123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Jack E.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10437963
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO: 46232
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: 701130375_FLI.pep
; US-10-437-963-126718

```

```

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Bing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 126718
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_29238C.1.pep
US-10-437-963-126718

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Query Match          25.0%; Score 5; DB 16; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  PRGAP 5
           |||||
Db      46  PRGAP 50

```

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RESULT 75
US-09-833-245-280
; Sequence 280, Application US/09833245
; Publication No. US2004010103A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCM
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 280
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-280

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```

Query Match          25.0%; Score 5; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  PRGAP 5
           |||||
Db      81  PRGAP 85

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Search completed: October 26, 2004, 07:47:56
Job time : 66 secs

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Result No.	Score	Query Match	Length	DB ID	Description
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1	6	30.0	324	4 US-08-948-113D-34	Sequence 34, Appli
2	5	25.0	9	1 US-07-972-032-15	Sequence 15, Appli
3	5	25.0	9	3 US-08-642-255-15	Sequence 15, Appli
4	5	25.0	46	3 US-09-124-671-6	Sequence 6, Appli
5	5	25.0	74	3 US-09-134-01IC-3074	Sequence 3074, Appli
6	5	25.0	74	3 US-09-134-01IC-4851	Sequence 4851, Appli
7	5	25.0	77	4 US-09-270-767-336912	Sequence 36912, Appli
8	5	25.0	77	4 US-09-270-767-52129	Sequence 52129, Appli
9	5	25.0	80	3 US-09-461-697-464	Sequence 464, Appli
10	5	25.0	91	4 US-09-552-991A-24182	Sequence 24182, Appli
11	5	25.0	91	4 US-09-270-767-38667	Sequence 38667, Appli
12	5	25.0	133	4 US-09-210-767-53884	Sequence 53884, Appli
13	5	25.0	105	4 US-09-489-09A-13486	Sequence 13486, Appli
14	5	25.0	109	3 US-09-124-671-21	Sequence 21, Appli
15	5	25.0	119	4 US-09-489-09A-11951	Sequence 11951, Appli
16	5	25.0	125	4 US-09-270-767-34003	Sequence 34903, Appli
17	5	25.0	125	4 US-09-270-767-50120	Sequence 50120, Appli
18	5	25.0	133	4 US-09-232-991A-30594	Sequence 30594, Appli
19	5	25.0	139	4 US-09-270-767-339768	Sequence 339768, Appli
20	5	25.0	139	4 US-09-270-767-54985	Sequence 54985, Appli
21	5	25.0	160	4 US-09-352-991A-23175	Sequence 232275, Appli
22	5	25.0	163	4 US-09-134-00C-3710	Sequence 3710, Appli
23	5	25.0	169	4 US-09-489-09A-8914	Sequence 8944, Appli
24	5	25.0	183	4 US-09-252-991A-23850	Sequence 21850, Appli
25	5	25.0	185	4 US-09-252-991A-32100	Sequence 32100, Appli
26	5	25.0	199	4 US-09-270-767-47191	Sequence 47191, Appli
27	5	25.0	212	4 US-09-252-991A-26521	Sequence 26521, Appli
28	5	25.0	29	4 US-09-270-767-60336	Sequence 60336, A
29	5	25.0	30	4 US-09-232-991A-23104	Sequence 23304, A
30	5	25.0	31	4 US-09-114-00IC-4115	Sequence 4165, Appli
31	5	25.0	32	4 US-09-232-991A-28143	Sequence 28143, A
32	5	25.0	32	4 US-08-456-819A-37	Sequence 37, Appli
33	5	25.0	34	4 US-09-248-796A-27518	Sequence 27518, A
34	5	25.0	35	4 US-09-253-991A-21517	Sequence 21517, A
35	5	25.0	35	4 US-09-710-279-1482	Sequence 1482, Appli
36	5	25.0	36	4 US-09-312-387B-8	Sequence 8, Appli
37	5	25.0	37	4 US-08-633-426-8	Sequence 8, Appli
38	5	25.0	38	4 US-08-633-458-8	Sequence 8, Appli
39	5	25.0	39	4 US-08-878-360-8	Sequence 8, Appli
40	5	25.0	39	4 US-09-33-412-8	Sequence 8, Appli
41	5	25.0	41	4 US-10-007-267-8	Sequence 6, Appli
42	5	25.0	42	4 US-08-312-387B-6	Sequence 6, Appli
43	5	25.0	42	4 US-08-633-426-6	Sequence 6, Appli
44	5	25.0	44	4 US-08-633-458-6	Sequence 6, Appli
45	5	25.0	45	4 US-08-878-360-6	Sequence 6, Appli
46	5	25.0	46	4 US-0-478-14DB-6	Sequence 6, Appli
47	5	25.0	47	4 US-09-33-412-6	Sequence 6, Appli
48	5	25.0	48	4 US-09-338-941-6	Sequence 6, Appli
49	5	25.0	49	4 US-10-007-267-6	Sequence 6, Appli
50	5	25.0	50	4 US-08-789-669A-2	Sequence 6, Appli
51	5	25.0	51	4 US-10-138-701-16	Sequence 6, Appli
52	5	25.0	52	4 US-09-232-991A-2676	Sequence 2676, A
53	5	25.0	53	4 US-09-253-991A-25496	Sequence 25496, A
54	5	25.0	54	4 US-09-53-110-5101	Sequence 5101, A
55	5	25.0	55	4 US-09-304-401-101	Sequence 2, Appli
56	5	25.0	56	4 US-09-304-615-106	Sequence 106, Appli
57	5	25.0	57	4 US-10-138-701-16	Sequence 16, Appli
58	5	25.0	58	4 US-09-134-001C-4824	Sequence 4824, Appli
59	5	25.0	59	4 US-09-252-991A-27119	Sequence 19369, A
60	5	25.0	60	4 US-09-252-991A-19369	Sequence 19369, A
61	5	25.0	61	4 US-09-252-991A-32186	Sequence 32186, A
62	5	25.0	62	4 US-09-252-991A-19891	Sequence 19891, A
63	5	25.0	63	4 US-09-270-767-46534	Sequence 46534, A
64	5	25.0	64	4 US-09-253-991A-20554	Sequence 20554, A
65	5	25.0	65	4 US-09-252-991A-17858	Sequence 17858, A
66	5	25.0	66	4 US-09-232-991A-31139	Sequence 31139, A
67	5	25.0	67	4 US-09-253-991A-231047	Sequence 231047, A
68	5	25.0	68	4 US-09-252-991A-13344	Sequence 19344, A
69	5	25.0	69	4 US-09-232-991A-26116	Sequence 26116, A
70	5	25.0	70	4 US-09-252-991A-30428	Sequence 30428, A
71	5	25.0	71	4 US-09-28-352-5815	Sequence 5815, Appli
72	5	25.0	72	4 US-09-396-218-2	Sequence 2, Appli
73	5	25.0	73	4 US-08-760-116-2	Sequence 2, Appli
74	5	25.0	74	4 US-09-196-982-5	Sequence 5, Appli
75	5	25.0	75	4 US-08-553-650A-5	Sequence 5, Appli
76	5	25.0	76	4 US-09-252-291A-19054	Sequence 19054, A
77	5	25.0	77	4 US-09-252-291A-27023	Sequence 27023, A
78	5	25.0	78	4 US-09-252-991A-55619	Sequence 25619, A
79	5	25.0	79	4 US-09-252-991A-32407	Sequence 32407, A
80	5	25.0	80	4 US-09-252-991A-1361	Sequence 21361, A
81	5	25.0	81	4 US-09-196-982-9	Sequence 9, Appli
82	5	25.0	82	4 US-08-653-650A-9	Sequence 9, Appli
83	5	25.0	83	4 US-09-252-991A-23505	Sequence 23505, A
84	5	25.0	84	4 US-09-252-991A-18255	Sequence 18255, A
85	5	25.0	85	4 US-09-252-991A-27602	Sequence 27602, A
86	5	25.0	86	4 US-09-13-53-11	Sequence 11, Appli
87	5	25.0	87	4 US-10-14-002-58	Sequence 4242, Appli
88	5	25.0	88	4 US-09-252-991A-25438	Sequence 25438, A
89	5	25.0	89	4 US-09-096-982-B	Sequence 9, Appli
90	5	25.0	90	4 US-08-153-650A-8	Sequence 8, Appli
91	5	25.0	91	4 US-08-12-916C-11	Sequence 11, Appli
92	5	25.0	92	4 US-08-807-342B-2	Sequence 2, Appli
93	5	25.0	93	4 US-09-13-53-11	Sequence 11, Appli
94	5	25.0	94	4 US-09-128-4424	Sequence 4424, Appli
95	5	25.0	95	4 US-09-252-991A-24711	Sequence 24711, A
96	5	25.0	96	4 US-09-54-681-6892	Sequence 6892, Appli
97	5	25.0	97	4 US-09-252-991A-29502	Sequence 29502, A
98	5	25.0	98	4 US-09-61-389-43	Sequence 43, Appli
99	5	25.0	99	4 US-10-14-002-10	Sequence 14, Appli
100	5	25.0	100	4 US-09-252-991A-17429	Sequence 17429, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

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No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

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No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-08-948-113D-34
; Sequence 34, Application US/08948113D
; Patent No. 6,482,937
; GENERAL INFORMATION:
; APPLICANT: Baetscher, Manfred W.
; APPLICANT: Akiyoshi, Donna E.
; APPLICANT: Kaplan, Ruth A.
; TITLE OF INVENTION: Pluripotent Porcine Cells, Genetically Modified Porcine Cells and Pigs for Use in Said Method, Transgenic Pigs
; FILE REFERENCE: 61750-309
; CURRENT APPLICATION NUMBER: US/08/948,113D
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 34
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Mus sp.
US-08-948-113D-34

Query Match 30.0%; Score 6; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 IETMFL 20
Db 210 IETMFL 215

RESULT 2
US 07-972-032-15
; Sequence 15, Application US/07972032
; Patent No. 5,466,712
; GENERAL INFORMATION:
; APPLICANT: Cappellico, Joseph A.
; APPLICANT: Ferrari, Franco A.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertram I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: CA 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A5556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-642-255-15

Query Match 25.0%; Score 5; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 5 PRGAP 9

RESULT 4
US-09-124-671-6
; Sequence 6, Application US/09124671A
; Patent No. 6,160,088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James

TELEPHONE: (415) 751-1939
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: fastSEQ for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Xenopus laevis
; SEQ ID NO: 671-6

Query Match 25.0%; Score 5; DB 3; Length 46;
Best Local Similarity 100.0%; Pred. No. 58; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 16 ETMFL 20
Db 31 ETMFL 35

RESULT 5
US-09-134-001C-3074
; Sequence 3074, Application US/09134001C
; Patent No. 6780370
GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTIC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 3074
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; SEQ ID NO: 134-001C-3074

Query Match 25.0%; Score 5; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 85; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 PRGAP 5
Db 58 PRGAP 62

RESULT 6
US-09-134-001C-4851
; Sequence 4851, Application US/09134001C
; Patent No. 6780370
GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTIC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 4851
; LENGTH: 74
; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis
; SEQ ID NO: 134-001C-4851

Query Match 25.0%; Score 5; DB 3; Length 74;
Best Local Similarity 100.0%; Pred. No. 85; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 PRGAP 5
Db 58 PRGAP 62

RESULT 7
US-09-270-767-36912
; Sequence 36912, Application US/09270767
; Patent No. 6703491
GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SEQ ID NO: 36912
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; OTHER INFORMATION: Xaa means any amino acid
; SEQ ID NO: 270-767-36912

Query Match 25.0%; Score 5; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 87; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 PRGAP 5
Db 70 PRGAP 74

RESULT 8
US-09-270-767-52129
; Sequence 52129, Application US/09270767
; Patent No. 6703491
GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; NUMBER OF SEQ ID NOS: 62517
; SEQ ID NO: 52129
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; OTHER INFORMATION: Xaa means any amino acid
; SEQ ID NO: 270-767-52129

Query Match 25.0%; Score 5; DB 4; Length 77;
Best Local Similarity 100.0%; Pred. No. 87; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 PRGAP 5
Db 70 PRGAP 74

RESULT 9
US-09-461-697-464
; Sequence 464, Application US/09461697

; Patent No. 6277974
 ; GENERAL INFORMATION:
 ; APPLICANT: COGENE NEUROSCIENCE, Inc.
 ; SEQ ID NO: 38667
 ; LENGTH: 91
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-38667

Query Match 25.0%; Score 5; DB 4; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 PRGAP 5
 Db 65 PRGAP 69

RESULT 12

US-09-270-767-53884
 ; Sequence 53884, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 53884
 ; LENGTH: 91
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-53884

Query Match 25.0%; Score 5; DB 4; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 PRGAP 5
 Db 65 PRGAP 69

RESULT 10

US-09-252-991A-24182
 ; Sequence 24182, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO: 24182
 ; LENGTH: 91
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-24182

Query Match 25.0%; Score 5; DB 4; Length 91;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 2 RGAPM 6
 Db 37 RGAPM 41

RESULT 11

US-09-270-767-38667
 ; Sequence 38667, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17

Query Match 25.0%; Score 5; DB 4; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 11 VQML 15
 Db 21 VQML 25

RESULT 14
 US-09-124-671-21
 ; Sequence 21, Application US/09124671A
 ; Patent No. 6,60088
 ; GENERAL INFORMATION:
 ; APPLICANT: Bothman, James
 ; APPLICANT: Maynew, Mark
 ; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
 ; FILE REFERENCE: 31488
 ; CURRENT FILING DATE: 1998-07-29
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 21
 ; LENGTH: 109
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chimeric Xenopus laevis TSP4-KDEL

Query Match 25.0%; Score 5; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 50 PRGAP 54

RESULT 15
 US-09-489-039A-11951
 ; Sequence 11951, Application US/09489039A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Bretton et. al.
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO KLEBSIELLA
 ; FILE REFERENCE: 2709 20040401
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 11951
 ; LENGTH: 119
 ; TYPE: PRT
 ; ORGANISM: Klebsiella pneumoniae

Query Match 25.0%; Score 5; DB 4; Length 119;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 93 PRGAP 97

RESULT 16
 US-09-270-767-34903
 ; Sequence 34903, Application US/092707077
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et. al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270-767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 34903

Query Match 25.0%; Score 5; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 50 PRGAP 54

RESULT 17
 US-09-270-767-50120
 ; Sequence 50120, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et. al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270-767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 50120
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; FEATURE:
 ; OTHER INFORMATION: Xaa means any amino acid

Query Match 25.0%; Score 5; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 50 PRGAP 54

RESULT 18
 US-09-252-991A-30594
 ; Sequence 30594, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196-136
 ; CURRENT APPLICATION NUMBER: US/09/252-991A
 ; CURRENT FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 30594
 ; LENGTH: 133
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa

Query Match 25.0%; Score 5; DB 4; Length 133;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 50 PRGAP 54

```

Db 47 PRGAP 51
    ; PRIORITY: 1998-02-18
    ; PRIOR FILING DATE: 1998-02-18
    ; PRIOR APPLICATION NUMBER: US 60/094,190
    ; NUMBER OF SEQ ID NOS: 33142
    ; SEQ ID NO: 23275
    ; LENGTH: 160
    ; TYPE: PRT
    ; ORGANISM: Pseudomonas aeruginosa
    ; US-09-252-991A-23275

RESULT 19
Query Match 25.0%; Score 5; DB 4; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    ; Query 1 PRGAP 5
    ; Db 23 PRGAP 27

Db 57 PRGAP 61
    ; PRIORITY: 1998-03-17
    ; FILE REFERENCE: File Reference: 7326-094
    ; CURRENT APPLICATION NUMBER: US/09/270,767
    ; CURRENT FILING DATE: 1999-03-17
    ; NUMBER OF SEQ ID NOS: 62517
    ; SOFTWARE: PatentIn Ver. 2.0
    ; LENGTH: 139
    ; TYPE: PRT
    ; ORGANISM: Drosophila melanogaster
    ; FEATURE:
    ; OTHER INFORMATION: Xaa means any amino acid
    ; US-09-270-767-39768

Query Match 25.0%; Score 5; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    ; Query 1 PRGAP 5
    ; Db 57 PRGAP 61

RESULT 20
Query Match 25.0%; Score 5; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    ; Query 1 PRGAP 5
    ; Db 57 PRGAP 61

    ; PRIORITY: 1998-03-17
    ; FILE REFERENCE: File Reference: 7326-094
    ; CURRENT APPLICATION NUMBER: US/09/270,767
    ; CURRENT FILING DATE: 1999-03-17
    ; NUMBER OF SEQ ID NOS: 62517
    ; SOFTWARE: PatentIn Ver. 2.0
    ; SEQ ID NO: 54985
    ; LENGTH: 139
    ; TYPE: PRT
    ; ORGANISM: Drosophila melanogaster
    ; FEATURE:
    ; OTHER INFORMATION: Xaa means any amino acid
    ; US-09-270-767-54985

Query Match 25.0%; Score 5; DB 4; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    ; Query 1 PRGAP 5
    ; Db 57 PRGAP 61

RESULT 21
Query Match 25.0%; Score 5; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    ; Query 1 PRGAP 5
    ; Db 23 PRGAP 27

    ; PRIORITY: 1999-01-29
    ; FILE REFERENCE: 107196.136
    ; CURRENT APPLICATION NUMBER: US/09/252,991A
    ; CURRENT FILING DATE: 1999-02-18
    ; NUMBER OF SEQ ID NOS: 14442
    ; LENGTH: 169
    ; TYPE: PRT
    ; ORGANISM: Klebsiella pneumoniae
    ; US-09-489-039A-8944

Query Match 25.0%; Score 5; DB 4; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    ; Query 1 PRGAP 5
    ; Db 23 PRGAP 27

```


Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 90 PRGAP 94

RESULT 29
US-09-252-991A-23304
; Sequence 23304, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 23304
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23304

Query Match 25.0%; Score 5; DB 4; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 40 PRGAP 44

RESULT 30
US-09-134-001C-4165
; Sequence 4165, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 4165
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4165

Query Match 25.0%; Score 5; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VQML 15
Db 52 VQML 56

RESULT 31
US-09-252-991A-28343
; Sequence 28343, Application US/09252991A

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 28343
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28343

Query Match 25.0%; Score 5; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 23 PRGAP 27

RESULT 32
US-08-426-819A-37
; Sequence 37, Application US/08426819A
; Patent No. 5723318
; GENERAL INFORMATION:
; APPLICANT: Yamaguchi, No. 5723318omi
; APPLICANT: Kojima, Tetsuo
; APPLICANT: Oh-Eda, Masayoshi
; APPLICANT: Hattori, Kunihiro
; TITLE OF INVENTION: Genes Coding for Megakaryocyte
; TITLE OF INVENTION: Potentiator
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasach & Birch
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATE:
; APPLICATION NUMBER: US/08/426,819A
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 230-107P
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-9050
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2448 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-426-819A-37

Query Match 25.0%; Score 5; DB 4; Length 248;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 115 PRGAP 119

RESULT 33 US-09-248-796A-27518
 ; Sequence 27518, Application US/09248796A
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US/09/248,796A
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 27518
 ; LENGTH: 257
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-27518

Query Match 25.0%; Score 5; DB 4; Length 257;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 13 QMLET 17
 Db 180 QMLET 184

RESULT 34 US-09-252-991A-21547
 ; Sequence 21547, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenstein et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 21547
 ; LENGTH: 259
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-21547

Query Match 25.0%; Score 5; DB 4; Length 259;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 56 PRGAP 60

RESULT 35

US-09-710-279-1482
 ; Sequence 1482, Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PI0348005
 ; CURRENT APPLICATION NUMBER: US/09/710,279
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1482
 ; LENGTH: 276
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 US-09-710-279-1482

Query Match 25.0%; Score 5; DB 4; Length 276;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 11 VQML 15
 Db 89 VQML 93

RESULT 36 US-08-312-187B-8
 ; Sequence 8, Application US/08312387B
 ; Patent No. 5515553
 ; GENERAL INFORMATION:
 ; APPLICANT: Goeschlich, Emil C.
 ; TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Krauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/312,387B
 ; FILING DATE: July 7, 1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 279 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-312-187B-8

Query Match 25.0%; Score 5; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

Db 121 LETMF 125

RESULT 37 US-08-683-426-8

Sequence 8, Application US/08683426
 Patent No. 5705367

GENERAL INFORMATION:

APPLICANT: Gotschlich, Emil C.

TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack

STATE: New Jersey

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent-In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/683,426

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/312,387

FILING DATE: September 26, 1994

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 134521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-683-458-8

Query Match 25.0%; Score 5; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEX: 134521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-683-426-8

Query Match 25.0%; Score 5; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 600-1-095A

REFERENCE/DOCKET NUMBER: 600-1-095A

TELEPHONE: 201 487-5800

TELEX: 134521

STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent-In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/683,458

FILING DATE: September 26, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEX: 134521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-683-458-8

Query Match 25.0%; Score 5; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEX: 134521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-683-458-8

Query Match 25.0%; Score 5; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEX: 134521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 279 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-683-458-8

Query Match 25.0%; Score 5; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEX: 134521

Query Match 25.0%; Score 5; DB 1; Length 279;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Mismatches 0; Indels 0; Gaps 0;

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-095A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEX: 134521

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-095B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
 LENGTH: 279 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-78-364-B

Query Match Score 5; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 15 LETMF 19
 Db 121 LETMF 125

RESULT 40
 US-09-333-412-B
 Sequence 8; Application US/09333412
 Patent No. 6342382

GENERAL INFORMATION:
 APPLICANT: Gotschlich, Emil C.
 TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/007,267
 FILING DATE: 03-Dec-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/333,412
 FILING DATE: 15-Jun-1999
 APPLICATION NUMBER: US/10/007,267
 FILING DATE: July 7, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-095

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 279 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-10-007-267-B

Query Match Score 5; DB 4; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 15 LETMF 19
 Db 121 LETMF 125

RESULT 42
 US-08-312-387-B-6
 Sequence 6; Application US/08312387B

GENERAL INFORMATION:
 APPLICANT: Gotschlich, Emil C.
 TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEX: 201 343-1684
 TELEX: 133521

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 279 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-333-412-B

Query Match Score 5; DB 3; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;

ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 ZIP: 07601
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/312,387B
 FILING DATE: July 7, 1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-0955
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 280 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-312-387B-6

Query Match 25.0%; Score 5; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LETMF 19
 |||||
 Db 121 LETMF 125

RESULT 43
 US-08-683-426-6

Sequence 6, Application US/08683426
 Patent No. 57053367
 GENERAL INFORMATION:
 APPLICANT: Gotschlich, Emil C.
 TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klauber & Jackson
 STREET: 411 Hackensack Avenue
 CITY: Hackensack
 STATE: New Jersey
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/683,458
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/312,387
 FILING DATE: September 26, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-095A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 280 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-683-426-6

Query Match 25.0%; Score 5; DB 1; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LETMF 19
 |||||
 Db 121 LETMF 125

RESULT 45
US-08-878-360-6
Sequence 6, Application US/088788360
Patent No. 5,945,322
GENERAL INFORMATION:
APPLICANT: Gorschluch, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
CITY: Hackensack Avenue
STATE: New Jersey
ZIP: 07601
COMPUTER READABLE FORM:
COMPUTER: IBM PC Compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,360
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,426
FILING DATE:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 6000-1-095B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-878-360-6

Query Match Score 5; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19
Db 121 LETMF 125

RESULT 47
US-09-333-412-6
Sequence 6, Application US/09333412
Patent No. 6,342,382
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF OLIGOSACCHARIDES, AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
CITY: Hackensack Avenue
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
Patent No. 6,127,153
GENERAL INFORMATION:
APPLICANT: JOHNSON, KARL F.
APPLICANT: ROTH, STEPHEN
APPLICANT: BUCZALA, STEPHANIE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

Qy 15 LETMF 19
Db 121 LETMF 125

RESULT 46
US-08-478-140B-6
Sequence 6, Application US/08478140B
Patent No. 6,127,153
GENERAL INFORMATION:
APPLICANT: JOHNSON, KARL F.
APPLICANT: ROTH, STEPHEN
APPLICANT: BUCZALA, STEPHANIE L.
TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds

TELEFAX: 201 343-1684
 TELE: 133521
 INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 280 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-333-412-6

Query Match Similarity 25.0%; Score 5; DB 3; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19
 Db 121 LETMF 125

RESULT 48
 US-09-338-943-6
 Sequence 6, Application US/09338943
 Patent No. 6379933
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, KARL F.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: ROTH, STEPHEN
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: BUZZALA, STEPHANIE L.
 TITLE OF INVENTION: METHOD OF TRANSFERRING AT LEAST TWO
 TITLE OF INVENTION: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE, A
 TITLE OF INVENTION: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/338,943
 FILING DATE:
 REFERENCE/DOCKET NUMBER: 600-1-095

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521

INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 280 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-10-007-267-6

Query Match 25%; Score 5; DB 4; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19
 Db 121 LETMF 125

RESULT 50
 US-09-904-615-106
 Sequence 106, Application US/09904615
 Patent No. 6566325
 GENERAL INFORMATION:
 FILE REFERENCE: PZ032P1
 CURRENT APPLICATION NUMBER: US/09/904,615
 FILE OF INVENTION: 49 Human Secreted Proteins
 APPLICANT: Rosen et al.
 CURRENT FILING DATE: 2001-07-16
 PRIOR APPLICATION NUMBER: 09/511,554
 PRIOR FILING DATE: 2000-02-23
 PRIOR APPLICATION NUMBER: 60/097,917

Query Match 25.0%; Score 5; DB 3; Length 280;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19

```

; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: US-09/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 106
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: SITE
; NAME/KEY: SITR
; LOCATION: (283)
; OTHER INFORMATION: Xaa equals stop translation
US-09-098-015-106

Query Match 25.0%; Score 5; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PRGAP 5
Db     199  PRGAP 203

RESULT 51
US-09-252-991A-27676
; Sequence 27676, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; FILE REFERENCE: 107196..136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 27676
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27676

Query Match 25.0%; Score 5; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PRGAP 5
Db     96  PRGAP 100

RESULT 52
US-09-252-991A-25496
; Sequence 25496, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196..136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 25496
; LENGTH: 289

Query Match 25.0%; Score 5; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  PRGAP 5
Db     236  PRGAP 240

RESULT 53
US-09-328-352-7849
; Sequence 7849, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTCC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO: 7849
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7849

Query Match 25.0%; Score 5; DB 4; Length 297;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15  LEIMF 19
Db     172  LEIMF 176

RESULT 54
US-09-583-110-5101
; Sequence 5101, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO: 5101
; LENGTH: 304
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5101

Query Match 25.0%; Score 5; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      14  MLEIM 18
Db     111  MLEIM 115

```

RESULT 55
US-08-789-609A-2
Sequence 2, Application US/08789609A
GENERAL INFORMATION:
Patent No. 5827689

APPLICANT: Gentry, Daniel
APPLICANT: Lonsdale, John
APPLICANT: Pearson, Stewart
APPLICANT: Payne, David
TITLE OF INVENTION: No. 5827689el Fabb
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: GM50004
FILING DATE: 24-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030685
FILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38 891
REFERENCE/DOCKET NUMBER: GM50004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:

SEQUENCE FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-789-609A-2

SEQUENCE FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-789-609A-2

Query Match 25.0%; Score 5; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 15 LETMF 19
Db 45 LETMF 49

RESULT 56
US-09-108-517-2
Sequence 2, Application US/09108517

GENERAL INFORMATION:
Patent No. 6258934
APPLICANT: Gentry, Daniel
APPLICANT: Lonsdale, John
APPLICANT: Pearson, Stewart
APPLICANT: Payne, David
TITLE OF INVENTION: No. 6258934el Fabb
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA

Query Match 25.0%; Score 5; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 15 LETMF 19
Db 45 LETMF 49

RESULT 55
US-08-789-609A-2
Sequence 2, Application US/08789609A
GENERAL INFORMATION:
Computer Readable Form:
Computer: IBM Compatible
Operating System: DOS
Software: FastSEQ for Windows Version 2.0
Current Application Data:
Application Number: US/09/108.517
Filing Date:
Classification:
Prior Application Data:
Application Number: 08/789,609
Filing Date:
Attorney/Agent Information:
Name: Gimmi, Edward R
Registration Number: 38,891
Reference/Doctet Number: GM50004
Telecommunication Information:
Telephone: 610-270-4478
Telex:
Information for Seq ID No: 2:
Sequence Characteristics:
Length: 308 amino acids
Type: amino acid
Strandedness: single
Topology: linear
Molecule Type: protein
US-09-108-517-2

Query Match 25.0%; Score 5; DB 3; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 15 LETMF 19
Db 45 LETMF 49

RESULT 57
US-10-138-701-16
Sequence 16, Application US/10138701
Patent No. 6753149
General Information:
Applicant: Human Genome Sciences, Inc., et al.
Title of Invention: *Staphylococcus aureus genes and polypeptides*
File Reference: PB484
Current Application Number: US/10/138,701
Prior Filing Date: 2002-05-06
Prior Application Number: US/09/512,255A
Prior Filing Date: 2000-02-24
Prior Application Number: US 60/098,964
Prior Filing Date: 1998-09-01
Prior Application Number: US 60/009,861
Seq ID No 16
Prior Filing Date: 1996-01-05
Prior Application Number: PCT/ US99/19726
Prior Filing Date: 1999-08-31
Prior Application Number: US 60/098,964
Prior Filing Date: 1997-10-20
Number of Seq ID Nos: 61
Software: PatentIn version 3.0
Length: 308
Type: PRT
Organism: *Staphylococcus aureus*
US-10-138-701-16

Query Match 25.0%; Score 5; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 15 LETMF 19
Db 45 LETMF 49

Db 45 LETMF 49

RESULT 58
US-09-134-001C-4824
; Sequence 1969, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO: 4824
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

Query Match 25.0%; Score 5; DB 3; Length 311;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETMF 19
Db 48 LETMF 52

RESULT 59
US-09-252-991A-19219
; Sequence 19219, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 19219
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

Query Match 25.0%; Score 5; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 106 PRGAP 110

RESULT 60
US-09-252-991A-19369
; Sequence 1969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 19369
; LENGTH: 339
; TYPE: PRT

RESULT 61
US-09-252-991A-32186
; Sequence 32186, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 32186
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

Query Match 25.0%; Score 5; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 141 PRGAP 145

RESULT 62
US-09-252-991A-19891
; Sequence 19891, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 19891
; LENGTH: 339
; TYPE: PRT

Query Match 25.0%; Score 5; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 141 PRGAP 145

Query Match 25.0%; Score 5; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 141 PRGAP 145

i ORGANISM: Pseudomonas aeruginosa
i US-09-252-991A-19891

Query Match Score 5; DB 4; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 94 PRGAP 98

RESULT 63
US-09-270-767-46634
; Sequence 46634, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,167
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 622517
; SOFTWARE: PatentIn Ver. 2.0
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE: Xaa means any amino acid
US-09-270-767-46634

Query Match Score 5; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 APMMW 8
Db 165 APMMW 169

RESULT 64
US-09-252-991A-20554
; Sequence 20554, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 20554
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (116), (202), (214), (251)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.

Query Match Score 5; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 153 PRGAP 157

RESULT 65
US-09-252-991A-17858
; Sequence 17858, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 31139
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-31139

Query Match Score 5; DB 4; Length 363;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RGAPM 6
Db 50 RGAPM 54

RESULT 66
US-09-252-991A-31139
; Sequence 31139, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 31139
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-31139

Query Match Score 5; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 153 PRGAP 157

RESULT 67
US-09-252-991A-23047
; Sequence 23047, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 31139
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-31139

Query Match Score 5; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Parent No. 5695966
 GENERAL INFORMATION:
 APPLICANT: INVENTI, Augusto
 APPLICANT: BREME, Umberto
 APPLICANT: COLOMBO, Anna L.
 APPLICANT: HUTCHINSON, Charles R.
 APPLICANT: OTTEN, Sharee
 APPLICANT: SCOTTI, Claudio
 TITLE OF INVENTION: PROCESSES FOR PREPARING DOXORUBICIN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIKALDO, MARMELSTEIN, MURRAY & ORAM
 STREET: 655 Fifteenth Street, N. W., Suite 330 - G
 CITY: Washington Lobby
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-5701
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/760,116
 FILING DATE: 3-DEC-1996
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/396,218
 FILING DATE: 27-FEB-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: KITTS, Monica C.
 REGISTRATION NUMBER: 36,105
 REFERENCE/DOCKET NUMBER: PI615-6007
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/638-5000
 TELEFAX: 202/638-4810
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 422 amino acids
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/396,218
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: KITTS, Monica C.
 REGISTRATION NUMBER: 36,105
 REFERENCE/DOCKET NUMBER: PI615-5002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202/638-5000
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 422 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-396-218-2

Query Match Score 5; DB 1; Length 422;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 325 PRGAP 329

RESULT 74
 US-09-096-982-5
 Sequence 5, Application US/09096982
 Patent No. 5962293
 GENERAL INFORMATION:
 APPLICANT: Strohl, William R.
 APPLICANT: Dickens, Michael L.
 APPLICANT: Desanti, Charles L.
 TITLE OF INVENTION: METHOD OF PRODUCING DOXORUBICIN
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CALFEE, HALTER & GRISWOLD
 STREET: 800 Superior Avenue, Suite 1400
 CITY: Cleveland
 STATE: Ohio
 COUNTRY: USA
 ZIP: 44114-2688
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/096,982
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Golick, Mary E.
 REGISTRATION NUMBER: 34829
 REFERENCE/DOCKET NUMBER: 22727/00131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 216-241-0816
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 422 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

RESULT 73
 US-08-760-116-2
 Sequence 2, Application US/08760116
 GENERAL INFORMATION:
 APPLICANT: INVENTI, Augusto
 APPLICANT: BREME, Umberto
 APPLICANT: COLOMBO, Anna L.
 APPLICANT: HUTCHINSON, Charles R.
 APPLICANT: OTTEN, Sharee
 APPLICANT: SCOTTI, Claudio
 TITLE OF INVENTION: PROCESSES FOR PREPARING DOXORUBICIN
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIKALDO, MARMELSTEIN, MURRAY & ORAM LLP
 STREET: 655 Fifteenth Street, N. W., Suite 330 - G
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-5701
 COMPUTER READABLE FORM:

; MOLECULE TYPE: protein

; US-09-096-982-5

Query Match 25.0%; Score 5; DB 2; Length 422;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 PRGAP 5
 Db 325 PRGAP 329

RESULT 75

US-08-653-650A-5

; Sequence 5, Application US/08653650A

; Patent No. 5776830

; GENERAL INFORMATION:

; APPLICANT: Strohl, William R.

; APPLICANT: Dickens, Michael L.

; APPLICANT: Desanti, Charles J.

; TITLE OF INVENTION: METHOD OF PRODUCING DOXORUBICIN

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CALFEE, HALTER & GRISWOLD

; STREET: 800 Superior Avenue, Suite 1400

; CITY: Cleveland

; STATE: Ohio

; COUNTRY: USA

; ZIP: 44114-2688

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/653,650A

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Golrich, Mary E.

; REGISTRATION NUMBER: 34829

; REFERENCE/DOCKET NUMBER: 222727/00131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 216-622-8458

; TELEFAX: 216-241-0816

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 422 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-653-650A-5

Query Match 25.0%; Score 5; DB 2; Length 422;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 PRGAP 5
 Db 325 PRGAP 329

Search completed: October 26, 2004, 07:25:06
 Job time : 24.25 BECS

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OM protein - protein search, using sw mode1

Run on: October 26, 2004, 07:05:46 ; Search time 16.5 Seconds
(without alignments)
116.626 Million cell updates/sec

Title: US-10-066-965A-4
Perfect score: 20
Sequence: 1 PRGAPMWLRVCQMLETKFL 20

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : PIR_79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
* * * *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID

Result No.	Score	Query	Match	Length	DB	ID	Description
1	6	30.0	238	2	S75336		hypothetical protein shikimate 5-dehydratase
2	6	30.0	278	2	DB315		conserved hypothetical protein
3	6	30.0	421	2	A82744		sun protein VCO4
4	6	30.0	434	2	GB2372		hypothetical protein
5	6	30.0	767	2	T19590		hypothetical protein
6	6	30.0	3396	2	T22613		hypothetical protein
7	5	25.0	34	2	PQ0341		L protein - rabies L protein - rabies
8	5	25.0	34	2	PQ0163		hypothetical protein
9	5	25.0	70	2	T10008		granulocyte chemotactic protein
10	5	25.0	75	2	B54188		hypothetical protein
11	5	25.0	75	2	T26778		TN916 ORF8 homolog
12	5	25.0	76	2	AB1212		conserved hypothetical protein
13	5	25.0	77	2	P69219		probable thioredoxin
14	5	25.0	90	2	S69133		platelet factor 4
15	5	25.0	102	2	A72518		hypothetical protein
16	5	25.0	113	2	AF2744		hypothetical protein
17	5	25.0	114	2	A55010		neutrophil-activating protein
18	5	25.0	114	2	E97725		hypothetical protein
19	5	25.0	119	2	T08271		probable thioredoxin
20	5	25.0	119	2	T11049		hypothetical protein
21	5	25.0	123	2	D72579		conserved hypothetical protein
22	5	25.0	127	2	AI0329		probable bacteriophage
23	4	25.0	127	2	AB0154		spasmolytic protein
24	5	25.0	128	1	S12372		spasmolytic polypeptide
25	5	25.0	129	1	I553637		C-X-C chemokine ligand 11
26	5	25.0	132	2	A57325		hypothetical protein
27	5	25.0	142	2	GB2796		hypothetical core
28	5	25.0	147	2	T5031		hypothetical protein
29	5	25.0	148	2	AH1645		hypothetical protein

3.0	2	AD1594	25.0	25.0	DNATopology modul
3.1	2	D71295	162	165	hypothetical prote
3.2	2	F82743	165	165	probable lipoprote
3.3	5	167	2	AH1106	hypothetical prote
3.4	5	173	2	H581294	precorrin-8N decar
3.5	5	179	2	S58124	hypothetical prote
3.6	5	192	2	D69161	hypothetical prote
3.7	5	192	2	T46483	hypothetical prote
3.8	5	193	2	AH1855	delta large antigenic
3.9	5	195	1	SAV1DM	complement compone
4.0	5	195	1	QQEBC5	matrix (Mutt) family
4.1	5	199	1	BB7935	hypothetical prote
4.2	5	202	2	T46688	RNA-directed RNA p
4.3	5	202	2	D70935	hypothetical prote
4.4	5	206	2	T22697	delta large antigenic
4.5	5	218	2	S28710	HGIF2 protein prec
4.6	5	222	1	BB3304	conserved hypothetical
4.7	5	229	2	B95110	hypothetical prote
4.8	5	229	2	B81429	conserved hypothetical
4.9	5	233	2	B90122	hypothetical prote
5.0	5	239	2	T22697	hypothetical prote
5.1	5	240	2	T20657	hypothetical prote
5.2	5	247	2	BB3833	hypothetical prote
5.3	5	248	1	INDGPS	pulmonary surfacta
5.4	5	249	2	T05424	hypothetical prote
5.5	5	250	2	C70823	thioesterase - Str
5.6	5	253	2	S49055	hypothetical prote
5.7	5	253	2	G90275	nG protein - Rho
5.8	5	253	2	C98748	conserved hypothetical
5.9	5	254	2	T22698	hypothetical protein (Ad2
6.0	5	262	2	T22698	flagellar assembly
6.1	5	266	2	H83956	exodeoxyribonucleic
6.2	5	273	2	T2114	hypothetical prote
6.3	5	277	2	S15563	hypothetical prote
6.4	5	278	2	C69854	hypothetical prote
6.5	5	280	2	T27610	hypothetical prote
6.6	5	280	2	E70745	hypothetical prote
6.7	5	284	2	T25501	hypothetical prote
6.8	5	296	2	T24827	hypothetical prote
6.9	5	304	2	G72276	hypothetical prote
7.0	5	305	2	T29906	hypothetical prote
7.1	5	306	2	AD2202	transcription regula
7.2	5	308	2	H75049	hypothetical prote
7.3	5	317	2	T47110	probable 35 kDa ri
7.4	5	318	2	T33845	hypothetical prote
7.5	5	325	2	AB2574	hypothetical prote
7.6	5	325	2	AH1312	transcription regula
7.7	5	325	2	AH1684	probable lipid tra
7.8	5	325	2	T02347	recombination prot
7.9	5	330	2	C52935	oxidoreductase lim
8.0	5	334	2	R36586	hypothetical prote
8.1	5	335	2	T29932	conserved hypothet
8.2	5	335	2	C72038	ATP binding protein
8.3	5	342	2	AF3198	conserved hypothet
8.4	5	343	1	CG9211	hypothetical prote
8.5	5	348	2	A11889	unknown protein [i
8.6	5	351	2	D36761	hypothetical prote
8.7	5	355	2	T29932	histidinol-phospho
8.8	5	357	2	T24137	cytokinin, type
8.9	5	359	2	T13289	cyclin CCM1 - years
9.0	5	368	2	T40115	hypothetical prote
9.1	5	382	2	DB2264	probable exopolysa
9.2	5	387	2	JB0364	lactosylceramide a
9.3	5	388	2	T09489	hypothetical prote
9.4	5	389	1	A48329	hypothetical prote
9.5	5	390	2	A60093	probable integrase
9.6	5	393	2	S39383	uv excision repair
9.7	5	406	2	S39965	probable exopolymer
9.8	5	407	2	T00693	hypothetical prote
9.9	5	409	2	T47298	probable replicati
10.0	5	409	2	T24138	hypothetical prote

ALIGNMENTS

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1<:TMA>

A;Cross-references: UNIPROT:Q9PEV0; GB:AE003849; PIDN:AAF9373

A;Experimental source: strain 945c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A. Briones, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrer, H. C;Species: Synechocystis sp.

C;Variety: PCC 6803

A;Title: Sequence analysis of the unicellular cyanobacterium Synechocystis s.

C;Accession: S75336

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. O.; Okumura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-238 <RAN>

A;Cross-references: UNIPROT:P73223; EMBL:D90904; GB:AB001339; PIDN:BAA1725

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match Score 6; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETKFL 20
 Db 165 LETKFL 170

RESULT 2

DB3815 shikimate 5-dehydrogenase arod [Imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004

C;Accession: D83815

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirashima, D.; Emelinaeva, M.D.; Dragoi, I.; Sellers, P. J., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

A;Reference number: A83650; MUID:205125B2; PMID:11058132

A;Accession: D83815

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-278 <STC>

A;Cross-references: UNIPROT:Q9KD93; GB:AP001511; PIDN:BA000004

A;Experimental source: strain C-125

C;Genetics:

A;Gene: arod

C;Superfamily: Shikimate 5-dehydrogenase; shikimate dehydrogenase homology

Query Match Score 6; DB 2; Length 278;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETKFL 20
 Db 225 LETKFL 230

RESULT 3

AB2744 conserved hypothetical protein XF0928 [Imported] - Xylella fastidiosa (strain 945c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: A82744

R;Anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000

A;Reference number: A82515; MUID:2036717; PMID:1090347

A;Note: For a complete list of authors see reference number A59328 below

A;Accession: A82744

C;Accession: Pereira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Froeh R.J.D.; Junqueira, M.L.; Krieger, J.E.; Kitajima, J.P.; Martins, E.E.; Martins, E.M.F.; Marino, C.L.; Marques, M.V.; Menez, C.P.M.; Mirello, E.C.; Miyaki, C.Y.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.P.M.; Oliveira, R.C.; Palmeiro, D.A.; Rodrigues, V.; Rosa, A.J.de M.; Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki M.; Tsuhako, M.H.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A;ContentS: annotation

C;Genetics:

C;Gene: XF0928

C;Superfamily: hypothetical protein HI0624

RESULT 4

G82372 sun protein VC0044 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: G82372

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Fritchman, D.; Remington, J.M.; Salzberg, S.L.; Qin, H.; Dragoi, I.; Sellers, P. J., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: G82372

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-434 <HEI>

C;Superfamily: hypothetical protein HI0624

Query Match Score 6; DB 2; Length 434;

Best Local Similarity 100.0%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 APNMWLR 9
 Db 159 APNMWLR 164

RESULT 5

T19690 hypothetical protein C33G3_1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T19690

R;Matthews, L.

A;Submitted to the EMBL Data Library, August 1996

A;Reference number: Z19163

A;Accession: T19690
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-767 <WIL>
A;Cross-references: UNIPROT:Q93325; EMBL:Z78540; PIDN:CA01738.1; GSPDB:GN00028; CESS:C3
A;Experimental source: Clone C33G3
C;Genetics:
A;Gene: CESP:C33G3.1
A;Map position: X
A;Intcns: 57/3; 72/3; 95/1; 143/3; 240/3; 285/3; 336/3; 419/3; 585/2; 658/3; 690/3; 75/1
Query Match Similarity 30.0%; Score 6; DB 2; Length 767;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 QMLETK 18
Db 403 QMLETK 408

RESULT 6
T22613 hypothetical protein F54B3.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22613
R;McMurray, A.
Submitted to the EMBL Data Library, March 1995
A;Reference number: Z19589
A;Accession: T22613
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3396 <WIL>
A;Cross-references: UNIPROT:O62263; EMBL:Z48583; PIDN:CAA88472.1; GSPDB:GN00020; CESS:FS
A;Experimental source: Clone F54B3
C;Genetics:
A;Gene: CESP:F54B3.1
A;Map position: 2
A;Intcns: 52/3; 109/3; 269/1; 295/1; 432/1; 560/2; 747/2; 938/3; 1073/1; 1719/2; 1877/2
C;Superfamily: *Caenorhabditis elegans* hypothetical protein F54B3.1
Query Match Similarity 30.0%; Score 6; DB 2; Length 3396;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 QMLETK 18
Db 1962 QMLETK 1967

RESULT 7
PQ0341 L protein - rabies virus
C;Species: rabies virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PQ0341
R;Sacramento, D.; Badrane, H.; Bourhy, H.; Tordo, N.
J. Gen. Virol. 73, 1149-1158, 1992
A;Title: Molecular epidemiology of rabies virus in France: Comparison with vaccine strain
A;Reference number: PQ0340; PMID:92268873; PMID:1568319
A;Accession: PQ0341
A;Molecule type: mRNA
A;Residues: 1-34 <SAC>
A;Cross-references: UNIPROT:Q91P05; MUID:92268873; PMID:1568319
A;Note: this sequence was obtained from isolates: WR56, WR06, WR39, WR97, WR18, WR63, WR
C;Superfamily: rhabdovirus L protein

Query Match Similarity 25.0%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5

Db 21 PRGAP 25

RESULT 8
PQ0363 L protein - rabies virus (isolate WR17)
C;Species: rabies virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: PQ0363
R;Sacramento, D.; Badrane, H.; Bourhy, H.; Tordo, N.
J. Gen. Virol. 73, 1149-1158, 1992
A;Title: Molecular epidemiology of rabies virus in France: Comparison with vaccine strain
A;Reference number: PQ0340; PMID:92268873; PMID:1568319
A;Accession: PQ0363
A;Molecule type: mRNA
A;Residues: 1-34 <SAC>
A;Cross-references: UNIPROT:Q91P05
C;Superfamily: rhabdovirus L protein

Query Match Similarity 25.0%; Score 5; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5

Db 21 PRGAP 25

RESULT 9
T18008 hypothetical protein a506R - *Chlorella virus* PBCV-1
C;Species: *Chlorella virus* PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18008
R;Graves, M.V.; Van Bitten, J.L.
Submitted to the EMBL Data Library, May 1999
A;Reference number: T18008
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-70 <GRB>
A;Cross-references: UNIPROT:Q98556; EMBL:U42580; NID:94028896; PIDN: AAC96873.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Note: a506R

Query Match Similarity 25.0%; Score 5; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LRCVC 12

Db 54 LRCVC 58

RESULT 10
B54188 granulocyte chemotactic protein, GCP-2 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C;Accession: B54188
R;Proost, P.; Wuyts, A.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Opdenakker, G.; Van De
Biochemistry 32, 1010-1017, 1993
A;Title: Human and bovine granulocyte chemotactic protein-2: complete amino acid sequence
A;Reference number: A54188; PMID:9401982; PMID:8391943
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-75 <PRO>
A;Experimental source: MDBK cells
A;Note: sequence extracted from NCBI backbone (NCBIP:137967)
C;Superfamily: beta-thromboglobulin

Query Match 25.0%; Score 5; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Residues: 1-76 <GAA>
 A; Cross-references: UNIPROT:Q8Y820; GB:NC_003210; PIDN:GAC99176.1; GSDB:
 A; Experimentall source: strain EGD-e
 C; Genetics: Imo1098

Query Match 25.0%; Score 5; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Residues: 1-76 <GAA>
 A; Cross-references: UNIPROT:Q9YX21; DBDB:AP000063; NID:95105654; PIDN:BAA81129.1; PID:95105654; F69219

RESULT 11
 T26778 hypothetical protein Y40B1A.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-199 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T26778
 R;Harris, B.
 Submitted to the EMBL Data Library, December 1998
 A;Reference number: Z20264
 A;Accession: T26778
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-75 <WIL>
 A;Cross-references: UNIPROT:Q9XW29; EMBL:AL034392; PIDN:CAA22304.1; CESP:Y40B1A.1
 A;Experimental source: clone Y40B1A
 C;Genetics:
 A;Gene: CESP:Y40B1A.1
 A;Introns: 61/3

RESULT 12
 AB1212 TN916 CRF8 homolog Imo1098 [imported] - *Listeria monocytogenes* (strain EGD-e)
 C;Species: *Listeria monocytogenes*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AB1212
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaude, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fsihi, H.; Jones, D.M.; Karst, U.; Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; Makok, C.; Schlueter, T.; Simeos, N.; Tierrro, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative Genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AB1212
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-76 <GAA>
 A;Cross-references: UNIPROT:Q8Y820; GB:NC_003210; PIDN:GAC99176.1; PID:916410500; GSDB:
 A;Experimentall source: strain EGD-e
 C; Genetics: Imo1098

Query Match 25.0%; Score 5; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Residues: 1-77 <WTH>
 A; Cross-references: UNIPROT:O26981; GB:AE0000865; NID:AE000666; PIDN:AAB8539

RESULT 13
 F69219 conserved hypothetical protein MTH895 - *Methanobacterium thermoautotrophicum* (strain Del)
 C;Species: *Methanobacterium thermoautotrophicum*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: F69219
 R;Smith, D.R.; Doucette-Stamm, L.A.; DeLoughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mac, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: funct
 A;Reference number: A69000; MUID:98037514; PMID:9371463
 A;Accession: F69219
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-77 <WTH>
 A; Cross-references: UNIPROT:O26981; GB:AE0000865; NID:AE000666; PIDN:AAB8539
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH895
 C;Superfamily: probable glutaredoxin grx-2
 Query Match 25.0%; Score 5; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: MTH895
 C;Superfamily: probable glutaredoxin grx-2
 Query Match 25.0%; Score 5; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: MTH895
 C;Superfamily: probable glutaredoxin grx-2
 Query Match 12 COMIE 16
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: MTH895
 C;Superfamily: probable glutaredoxin grx-2
 Query Match 14 COMIE 18
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: MTH895
 C;Superfamily: probable glutaredoxin grx-2
 RESULT 14
 S69133 platelet factor 4 - pig
 C;Species: *Sus scrofa domesticus* (domestic Pig)
 C;Date: 10-Mar-1998 #sequence_revision 10-Mar-1998 #text_change 09-Jul-2004
 C;Accession: S69133
 R;Proudfoot, A.E.I.; Magnenat, E.J.; Halley, T.M.; Maiione, T.E.; Wells, T.N.C.
 Eur. J. Biochem. 228, 658-664, 1995
 A;Title: The complete primary structure of glycosylated porcine platelet factor 4.
 A;Reference number: S69133; MUID:95255268; PMID:7737160
 A;Accession: S69133
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-90 <PRO>
 A;Cross-references: UNIPROT:P20034
 A;Note: blocked N-terminus
 C;Superfamily: beta-thromboglobulin
 Query Match 25.0%; Score 5; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: S69133
 C;Superfamily: beta-thromboglobulin
 Query Match 25.0%; Score 5; DB 2; Length 90;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: S69133
 C;Superfamily: beta-thromboglobulin
 Query Match 8 IRCV 12
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: S69133
 C;Superfamily: beta-thromboglobulin
 Query Match 8 IRCV 12
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: S69133
 C;Superfamily: beta-thromboglobulin
 Query Match 23 IRCV 27
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 A; Gene: S69133
 C;Superfamily: beta-thromboglobulin
 RESULT 15
 A72518 hypothetical protein APE2118 - *Aeropyrum pernix* (strain K1)
 C;Species: *Aeropyrum pernix*
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C;Accession: A72518
 R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K. DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyrum pernix*
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: A72518
 A;Molecule type: DNA
 A;Residues: 1-102 <YAW>
 A; Cross-references: UNIPROT:Q9YX21; DBDB:AP000063
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE2118

C;Superfamily: *Aeropyrum pernix* hypothetical protein APE2118
 Query Match 25.0%; Score 5; DB 2; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 APWML 8
 Db 35 APWML 39

RESULT 16
 AF2744 hypothetical protein Atul366 [imported] - *Agrobacterium tumefaciens* (strain C58, Dupont)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C;Accession: AF2744
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2322, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A;Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A;Reference number: AB2577; PMID:21608550; PMID:11743193
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atul366
 A;Map position: circular chromosome
 Query Match 25.0%; Score 5; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 PWMLR 9
 Db 71 PWMLR 75

RESULT 17
 A55010 neutrophil-activating peptide ENA-78 precursor - human
 N;Alternate names: epithelial-derived neutrophil-activating peptide 78 (ENA-78)
 C;Species: Homo sapiens (man)
 C;Date: 11-Nov-1994 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C;Accession: JC2433; A55010; I37357; JH058; PS0347; S4075
 R;Corbett, M.S.; Schmitt, J.; Riess, O.; Walz, A.
 Biochem. Biophys. Res. Commun. 205, 612-617, 1994
 A;Title: Characterization of the gene for human neutrophil-activating peptide 78 (ENA-78)
 A;Reference number: JC2433; PMID:95091791; PMID:7939089
 A;Accession: JC2433
 A;Molecule type: DNA
 A;Residues: 1-114 <COR>
 A;Cross-references: UNIPROT:PA2830; GB:L37036; PID:g607030; PID:g607031
 R;Chang, M.; McNinch, J.; Basu, R.; Simonet, S.
 J. Biol. Chem. 269, 2527-2528, 1994
 A;Title: Cloning and characterization of the human neutrophil-activating peptide (ENA-78)
 A;Reference number: A55010; PMID:95014315; PMID:7939219
 A;Accession: A55010
 A;Molecule type: DNA
 A;Residues: 1-12, S, 14-114 <CHA>
 A;Cross-references: GB:U12209
 R;Power, C.A.; Furness, R.B.; Brawand, C.; Wells, T.N.
 Gene 151, 333-334, 1994
 A;Title: Cloning of a full-length cDNA encoding the neutrophil-activating peptide ENA-78
 A;Reference number: I37357; PMID:95129887; PMID:7828901
 A;Accession: I37357
 A;Status: translated from GB/EMBL/DDJB

C;Superfamily: *Aeropyrum pernix* hypothetical protein APE2118
 A;Molecule type: mRNA
 A;Residues: 1-114 <RES>
 A;Cross-references: EMBL:X78686; NID:9471242; PID:9471243
 R;Walz, A.; Burgener, R.; Car, B.; Baggolini, M.; Kunkel, S.L.; Strieer, R.M.
 J. Exp. Med. 174, 135-1362, 1991
 A;Title: Structure and neutrophil-activating properties of a novel inflammatory peptide
 A;Reference number: JH0556; PMID:92078844; PMID:1744577
 A;Accession: JH0556
 A;Molecule type: mRNA
 A;Residues: 43-114 <WALL>
 A;Experimental source: pulmonary type II epithelial cell line A549
 A;Accession: PS0347
 A;Molecule type: protein
 A;Residues: 37-70;93-114 <WALL>
 C;Genetics:
 A;Gene: ENA78; NAP
 A;Map position: 4q13-q21
 A;Introns: 37/1; 81/3; 109/2
 C;Superfamily: beta-thromboglobulin
 C;Keywords: cytokine
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:37-14/Product: neutrophil-activating Peptide ENA-78 #status experimental <MAT>
 Query Match 25.0%; Score 5; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 8 LRCVC 12
 Db 47 LRCVC 51

RESULT 18
 B97525 hypothetical protein AGR_C_2526 [imported] - *Agrobacterium tumefaciens* (strain C58, Cerec)
 C;Species: *Agrobacterium tumefaciens*
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: E97525
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ourollo, B.; Goldman, A.; Liu, F.; Wellam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 293, 2333-2338, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A;Reference number: 297359; PMID:21608551; PMID:11743194
 A;Accession: E97525
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-114 <KTR>
 A;Cross-references: UNIPROT:Q8UFN1; GB:AE007869; PID:AAK87158.1; PID:915156430; GSPDB:GN
 C;Genetics:
 A;Gene: AGR_C_2526
 A;Map position: circular chromosome
 Query Match 25.0%; Score 5; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 PMWLR 9
 Db 72 PMWLR 76

RESULT 19
 T08271 probable thioredoxin - *Halobacterium* sp. (strain NRC-1) plasmid pNRC100
 N;Alternate names: hypothetical protein H0606; hypothetical protein H1757
 C;Species: Halobacterium sp.
 A;Variety: strain NRC-1
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T08271; T08372
 R;NG, W.V.; Ciuci, S.A.; Smith, T.M.; Bumgarner, R.E.; Faust, J.; Hall, B.; I Genome Res. 9, 1131-1141, 1998
 A;Title: Snapshot of a large dynamic replicon in a halophilic archaeon: megaplasmid or mJ
 A;Reference number: 216406; PMID:93063793; PMID:9847077

A;Accession: T08271
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-119 <NCW>
A;Cross-references: UNIPROT:046709; EMBL:AF016485; NID:92822278; PID:92822332; HALOSP:HO
A;Experimental source: strain NRC-1
C;Genetics:
A;Accession: T08372
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-119 <DSB>
A;Cross-references: EMBL:AF016485; NID:92822278; PID:92822433; HALOSP:HI757
A;Experimental source: strain NRC-1
C;Genetics: COP2
C;Genetics: <COP1>
A;Gene: LrXA; HALOSP:H0606
A;Genome: Plasmid pNRC100
C;Genetics: <COP2>
A;Gene: trXA; HALOSP:HI757
A;Genome: plasmid pNRC100
C;Function: involved in reduction of ribonucleotides, methionine sulfoxide sulfate, a
A;Description: involved in reduction of ribonucleotides, methionine sulfoxide sulfate, a
C;Superfamily: thioredoxin/thioredoxin/thioredoxin homology
Query Match 25.0%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586350

RESULT 22
AI0329
Conserved hypothetical protein YPO2705 [imported] - Yersinia pestis (strain C09
C;Species: Yersinia pestis
C;Accession: AI0329
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prent
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou
il, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586350

RESULT 23
AI0329
Conserved hypothetical protein YPO2705 [imported] - Yersinia pestis (strain C09
C;Species: Yersinia pestis
C;Accession: AI0329
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prent
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou
il, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586350

RESULT 23
YPO1259 [imported] - Yersinia pestis (strain C09
C;Species: Yersinia pestis
C;Accession: YPO1259
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prent
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou
il, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586350

RESULT 23
YPO1259 [imported] - Yersinia pestis (strain C09
C;Species: Yersinia pestis
C;Accession: YPO1259
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prent
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou
il, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586350

RESULT 23
D72579
Hypothetical protein APE1916 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Accession: D72579
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yanazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takami, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz
A;Reference number: A72450; MUID:10382966
A;Accession: D72579
Query Match 25.0%; Score 5; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A;Cross-references: UNIPROT:Q8ZGM8 ; GB:AL590842; PID:92865265; PID:NID:92865253;
A;Genome: mitochondrial
C;Keywords: mitochondrial
A;Molecule type: DNA
A;Residues: 1-119 <DSB>
A;Cross-references: UNIPROT:047553; EMBL:AF008237; NID:92865253; PID:92865265; PID:NID:92865253

RESULT 23
D72579
Hypothetical protein APE1916 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Accession: D72579
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yanazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takami, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.;
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyz
A;Reference number: A72450; MUID:10382966
A;Accession: D72579
Query Match 25.0%; Score 5; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MWLRC 5

RESULT 24

S12372
spasmodolytic protein precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-93 #sequence_revision 24-May-1996 #text_change 18-Jun-1999
C;Accession: S12372; S63997
R;Tomasetto, C.; Rio, M.C.; Gautier, C.; Wolf, C.; Harueveni, M.; Chambon, P.; Lathe, R.
EMBL J. 9; 407-414; 1990
A;Title: hsp, the domain-duplicated homolog of ps2 protein, is co-expressed with ps2 in
A;Reference number: S12371; MUID:90151615; PMID:2303034
A;Accession: S12372
A;Molecule type: mRNA
A;Residues: 1-128 <TOM>
A;Cross-references: EMBL:X51697
R;Tomasetto, C.; Rio, M.C.; Gautier, C.; Wolf, C.; Harueveni, M.; Chambon, P.; Lathe, R.
submitted to the EMBL Data Library, December 1993
A;Description: hsp, the domain-duplicated homolog of ps2 protein, is co-expressed with ps2 in
A;Reference number: S63997
A;Accession: S63997
A;Molecule type: mRNA
A;Residues: 1-10; V; 12-128 <TOW>
A;Cross-references: EMBL:X51697; NID:954165; PID:954166
C;Genetics:
A;Gene: msp
C;Function:
A;Description: inhibits gastrointestinal motility and gastric acid secretion
C;Superfamily: spasmodolytic protein; trefoil homology
C;Keywords: duplication; hormone; pancreas
F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F;23-128/Product: spasmodolytic protein #status predicted <MAT>
F;70-71/Domain: trefoil homology <TRFL>
F;80-120/Domain: trefoil homology <TRP2>
F;28-126;30-57;41-56;51-68;80-106;90-105;100-117/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 25.0%; Score 5; DB 1; Length 128;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 2 PRGAP 6

Qy

25.0%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 2 PRGAP 6

Qy

25.0%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 2 PRGAP 6

Qy

25.0%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 2 PRGAP 6

RESULT 25

T50331

RESULT 26

A57325
C-X-C chemokine LIX - mouse
C;Alternate names: Garg-8/LIX; glucocorticoid-attenuated response gene 8
C;Species: Mus musculus (house mouse)
C;Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 09-Jul-2004
C;Accession: A57325
R;Smith, J.B.; Herschman, H.R.
J. Biol. Chem. 270; 16756-16765; 1995
A;Title: Glucocorticoid-attenuated response genes encode intercellular mediators, includi
A;Reference number: A57325; MUID:95348101; PMID:7622488
A;Accession: A57325
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-132 <SM>
A;Cross-references: UNIPROT:Q50228; GB:U27267; NID:9950158; PID:9950159
C;Superfamily: beta-thromboglobulin

Query Match

25.0%; Score 5; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 LRCVC 12
Db 51 LRCVC 55

RESULT 27

G82796
hypothetical protein XP0524 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82796
R;Anonymous, The Xylella Fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406; 151-157; 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82796
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <SM>
A;Cross-references: UNIPROT:Q9PFY2; GB:AB003900; GB:AB003849; NID:99105366; PID:AAF83334

Qy

25.0%; Score 5; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A;Content: annotation
C;Genetics:
A;Reference number: A59328
A;Accession: V.C.A.; Ferreiro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laligre
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Alvarenga, R.; Aj
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carrasco, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.,
A;Authors: Ferreira, V.C.A.; Ferreiro, J.A.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laligre
A;Authors: Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.;
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, F.W.A.; da Silveira
M.; Tsuchiko, M.H.; Vallada, R.; Van Sluy, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze
A;Molecule type: mRNA
A;Residues: 1-129 <RES>

Qy

25.0%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 59 PRGAP 63

Qy

25.0%; Score 5; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 3 PRGAP 7

hypothetical coiled-coil protein [Imported] - fission yeast (*Schizosaccharomyces pombe*)
 C;Species: *Schizosaccharomyces pombe*
 C;Date: 09-Jun-2000 #text_change 09-Jun-2000 #text_revision 09-Jul-2004
 C;Accession: T50331
 R;Lynne, M.A.; Rayandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
 submitted to the EMBL Data Library, February 2000
 A;Reference number: Z25062
 A;Status: preliminary; translated from GB/EMBL/DDDBJ
 A;Molecule type: DNA
 A;Residues: 1-147 <LYN>
 A;Cross-references: UNIPROT:Q9P7P1; EMBL:AL157874; PIDN:CAB75993.1; GSPDB:GN00067; SPDB:
 A;Experimental source: strain 972h(-); cosmid C1718
 C;Genetics:
 A;Gene: SPBC1718.03
 A;Map position: 2

Query Match 25.0%; Score 5; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 QMLET 18
 Db 86 MLETK 90

RESULT 29

AH1645 hypothetical protein lin1705 [Imported] - *Listeria innocua* (strain Clip11262)
 C;Species: *Listeria innocua*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AH1645
 R;Glaser, P.; Frangneul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurge, O.; Entian, K.D.; Fsihi, H.; Jones, I.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourna, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierre, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A.;Title: Comparative genomics of *Listeria* species.
 A;Reference number: A01077; MUID:215337279; PMID:11679669
 A;Accession: AH1645
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-148 <GLA>
 A;Cross-references: UNIPROT:Q92B45; GB:AL592022; PIDN:CAC96936.1; PID:916414192; GSPDB:G
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin1705

Query Match 25.0%; Score 5; DB 2; Length 148;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QMLET 17
 Db 11 QMLET 15

RESULT 32

F82743 hypothetical protein XF0947 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: D75295
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.R.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.; Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A;Reference number: A75250; MUID:2036896; PMID:10567266
 A;Accession: D75295
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-162
 A;Cross-references: UNIPROT:Q9RS54; GB:AE000513; PIDN:96460070; PIDN:AAF1181
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR2273
 A;Map position: 1

Query Match 25.0%; Score 5; DB 2; Length 162;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QMLET 17
 Db 133 QMLET 137

RESULT 32

F82743 hypothetical protein XF0947 [imported] - *Xylella fastidiosa* (strain 9a5c)

C;Species: *Xylella fastidiosa*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: F82743
 R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: A8251; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: F82743
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-165 <SLM>
 A;Cross-references: UNIPROT:Q9REBT1; GB:AE003943; PID:99105863; PID:99105849; PID:AE003849
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carrasco, D.M.; Carrer, H.; as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lages Martins, E.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marques, M.V.; Marino, C.I.; Miracca, B.C.; Miyaki, C.Y.;
 A;Authors: Ferreira, V.C.; Franco, M.C.; Frohnmayer, J.A.; Ferro, J.S.; Krieger, J.E.; Junqueira, M.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lages Martins, E.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marques, M.V.; Marino, C.I.; Miracca, B.C.; Miyaki, C.Y.,
 A;Accession: AD1594

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A; Rodrigues, R.; Rosa, V.E.; de Sa, R.G.; Sant'ana, R.V.; Savausk M.; Tsuhako, M.H.; Vallada, H.; da Silva, A.M.; Silva Jr., W.A.; da Silveir A; Reference number: A59328
A; Contents: annotation
C; Genetics:
A; Gene: XF0947

Query Match Score 5; DB 2; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 7 WLRCV 11
Db 144 WLRCV 148

RESULT 33
AH1106 hypothetical protein lmo0255 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1106
R;Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ; Dominguez-Bernal, G.; Duchaud, B.; Durand, L.; Dussurgeot, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kunin, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schlueter, T.; Simoes, N.; Tierraz, A.; Vazquez-Boland, J.A.; Voss, H.; Weiland, A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679659
A;Accession: AH1106
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <GLA>
A;Cross-references: UNIPROT:QBYA99; GB:NC_003210; PIDN:CAD00782.1; PID:gi16409620; GSDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo0255

Query Match Score 5; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Qy 15 LETKF 19
Db 110 LETKF 114

RESULT 34
H81294 probable lipoprotein Cj1483c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Accession: HB1294
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, A.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: HB1294
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <PAR>
A;Cross-references: UNIPROT:Q9PMH9; GB:AL111168; PID:gi6968723; PIDN:CAB390
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1483c
C;Superfamily: Campylobacter jejuni probable lipoprotein Cj1483c
Query Match Score 5; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

A;Reference number: Z23035
A;Accession: T46483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-192 <AAA>
A;Cross-references: UNIPROT:Q969U6; EMBL:AL137631
A;Experimental source: adult testis; clone DKFZp434B205
C;Genetics:
A;Note: DKFZp434B205.1

Db 159 PRGAP 163

|||||

RESULT 4
SAVLDS
delta large antigen - hepatitis delta virus (isolate Japanese S-1)
N;Alternate names: HDag
C;Species: hepatitis delta virus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B36409; S18678
R;Imareki, F.; Omata, M.; Ohto, M.
J;Virol. 64, 5594-5599, 1990
A;Title: Heterogeneity and evolution rates of delta virus RNA sequences.
A;Reference number: A36409; MUID: 91012805; PMID: 2214027
A;Accession: B36409
A;Molecule type: genomic RNA
A;Residues: 1-195 <IMAI>
A;Cross-references: UNIPROT:P25883; GB:D90192; GB:M58303; NID:q221695; PIDN:BAA14216.1;
A;Experimental source: isolate Japanese S-1
R;Imareki, F.; Omata, M.; Ohto, M.
Nucleic Acids Res. 19, 5439, 1991
A;Title: Complete nucleotide sequence of hepatitis delta virus RNA in Japan.
A;Accession: S18678
A;Reference number: 92020244; PMID: 1923832
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: genomic RNA
A;Residues: 1-195 <IMAI2>
A;Cross-references: EMBL:X60193; NID:g59497; PIDN:CAA42749.1; PMID:g59498
A;Experimental source: isolate Japanese S-1
A;Note: note this sequence was submitted to the EMBL Data Library, June 1991
C;Superfamily: hepatitis delta virus large antigen
C;Keywords: core protein
F;2-195/Product: delta large antigen #status predicted <MAR>

Query Match Score 5; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 MLETK 18
Db 137 MLETK 141

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RESULT 38
AH1855
hypothetical protein al10393 [Imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH1855
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchishi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID: 21595285; PMID: 11759840
A;Accession: AH1855
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <AAA>
A;Cross-references: UNIPROT:Q8YZR4; GB:BA000019; PIDN:BAB72351.1; PID:917129738; GSPDB:G
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: al10393

Query Match Score 5; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETKEFL 20
Db 114 ETKEFL 118

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RESULT 39
SAVLDS
delta large antigen - hepatitis delta virus (strain Japanese M-1)
N;Alternate names: HDag
C;Species: hepatitis delta virus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A36409
R;Imareki, F.; Omata, M.; Ohto, M.
J;Virol. 64, 5594-5599, 1990
A;Title: Heterogeneity and evolution rates of delta virus RNA sequences.
A;Reference number: A36409; MUID: 91012805; PMID: 2214027
A;Accession: A36409
A;Molecule type: genomic RNA
A;Residues: 1-195 <IMAI>
A;Cross-references: UNIPROT:P25881; GB:D90190; GB:M58299; NID:q221691; PIDN:BAA14214.1;
C;Superfamily: hepatitis delta virus large antigen
C;Keywords: core protein
F;2-195/Product: delta large antigen #status predicted <MAT>

Query Match Score 5; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5

RESULT 44
 A;Gene: HQLF2
 C;Superfamily: cytomegalovirus HQLF2 protein
 C;Keywords: glycoprotein, transmembrane protein
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-198/Domain: hypothetical protein US2 #status predicted <MM>
 F;161-186/Domain: transmembrane #status predicted <MM>
 F;68/Binding site: carbohydrate (Asn) (covalent) #status predicted <MM>

Query Match Score 5; DB 1; Length 199;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WLRCV 11
 Db 130 WLRCV 134

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F;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Accession: D70935
 A;Molecule type: DNA
 A;Residues 1-206 <CCD>
 A;Cross-references: UNIPROT:O53504; GB:AL021957; PMID:93242293; PIDN:CAA17474
 A;Experimental source: strain H37Rv
 C;Genetics:
 P;Gene: Rv2170

RESULT 42
 I46688
 complement component C8 gamma subunit - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Accession: I46688
 R;White, R.V.; Kaufman, K.M.; Letson, C.S.; Platteborze, P.L.; Sodetz, J.M.
 J. Immunol. 152, 2501-2508, 1994
 A;Title: Characterization of rabbit complement component C8: Functional evidence for the A;Reference number: I46686; MUID:94179833; PMID:7510745
 A;Accession: I46688
 A;Molecule type: mRNA
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Residues: 1-202 <NH1>
 C;Super-references: UNIPROT:Q28679; GB:L26979; NID:9469064; PIDN:AAA31193.1; PID:9469065
 F;42-188/Domain: lipocalin homology <LIP>
 Query Match Score 5; DB 2; Length 202;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 26 PRGAP 30

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Query Match Score 5; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AFMWL 8
 Db 39 AFMWL 43

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RESULT 45
 S28710
 RNA-directed RNA polymerase homolog - sugar beet yellow virus (fragment)
 C;Species: sugar beet yellow virus, SBV
 C;Date: 07-May-1993 #sequence_revision 07-May-1993
 C;Accession: S28710
 E;Agranovsky, A.A.; Boyko, V.P.; Karasev, A.V.; Lunina, N.A.; Koonin, E.V.; Dolja, V.V.
 J. Gen. Virol. 72, 15-23, 1991
 A;Title: Nucleotide sequence of the 3'-terminal half of beet yellows closterovirus RNA 9c
 A;Reference number: S28710; MUID:91116305; PMID:1990061
 A;Accession: S28710
 A;Molecule type: DNA
 A;Residues 1-218 <AGR>
 A;Cross-references: EMBL:X53462; NID:958878; PIDN:CAA37549.1; PID:9808947

Query Match Score 5; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETKFL 20
 Db 64 ETKFL 68

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RESULT 46
 S33204
 hypothetical protein - long-stalked stichwort
 C;Species: Stellaria longipes (long-stalked stichwort)
 C;Date: 09-Jun-1994 #sequence_revision 12-May-1995
 C;Accession: S33204
 P;Zhang, X.H.
 Submitted to the EMBL Data Library, April 1993

Query Match Score 5; DB 2; Length 202;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ETKFL 20
 Db 14 ETKFL 18

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RESULT 49
 Qy 1 PRGAP 5
 Db 54 PRGAP 58

RESULT 47
 B95910 conserved hypothetical protein Smb20806 [imported] - Sinorhizobium meliloti (strain 1021)
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: B95910
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci., U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; PMID:21396508; PMID:11481431
 A;Accession: B95910
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-229 <KUR>
 A;Cross-references: UNIPROT:Q92W01; GB:AU591985; PIDN:CAAC48946_1; PID:915140431; GSDB:G
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 peila, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 291, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Koml, C.; Lelaurae,
 hebuilt, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Content: annotation
 C;Genetics:
 A;Gene: Smb20806
 A;Genome: plasmid

Matches 5; Score 5; DB 2; Length 229;
 Qy 16 ETKFL 20
 Db 115 ETKFL 119

RESULT 48
 B81429 hypothetical protein Cj0122 [imported] - Campylobacter jejuni (strain NCTC 11168)
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: B81429
 R;Parikh, B.W.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
 Nature 403, 665-668, 2000
 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
 A;Reference number: A81250; PMID:20150912; PMID:10688204
 A;Accession: B81429
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-229 <PAR>
 A;Cross-references: UNIPROT:Q9PJP05; GB:AU139074; GB:AL11168; PIDN:96967505; PIDN:CA7260
 A;Experimental source: serotype O2, strain NCTC 11168
 C;Genetics:
 A;Gene: Cj0122

Matches 5; Score 5; DB 2; Length 229;
 Qy 15 LETKF 19
 Db 186 LETKF 190

RESULT 49
 B90222 conserved hypothetical protein [imported] - Sulfolobus solfataricus
 C;Species: Sulfolobus solfataricus
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: B90222
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V
 arrett, R.A.; Ragan, M.A.; Medina, N.; Peng, X.; Thi-Ngo, H.P.; Redder, P.
 submitted to GenBank, April 2001
 A;Description: Sulfolobus solfataricus complete genome.
 A;Reference number: A99139
 A;Accession: B90222
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-233 <KUR>
 A;Cross-references: UNIPROT:Q9UXC5; GB:AE006641; PIDN:AAK41033_1; GSDB:G
 C;Genetics:
 A;Gene: SS00737

Query Match 25/0%; Score 5; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 14 MLETK 18
 Db 95 MLETK 99

RESULT 50
 T29697 hypothetical protein F31A3.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T29697
 R;Murray, J.; Le, T.T.
 submitted to the EMBL Data Library, May 1996
 A;Description: The sequence of C. elegans cosmid F31A3.
 A;Reference number: 220667
 A;Accession: T29697
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-239 <MR>
 A;Cross-references: UNIPROT:Q19917; EMBL:U58742; PIDN:AAB36858_1; GSDB:GN00028; CESP:
 C;Genetics:
 A;Experimental source: strain Bristol R2; clone F31A3
 A;Gene: CEPF:F31A3.4
 A;Map Position: X
 A;Introns: 57/2; 132/2

Query Match 25/0%; Score 5; DB 2; Length 239;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 LETKF 19
 Db 74 LETKF 78

RESULT 51
 T20657 hypothetical protein F09E8_1 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T20657
 R;Percy, C.
 submitted to the EMBL Data Library, May 1996
 A;Reference number: Z19307
 A;Accession: T20657
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-240 <WIL>

A;Cross references: UNIPROT:Q19268; EMBL:273896; PIDN:CAA98056..1; GSPDB:GN00022; CBSP:FO	A;Experimental source: clone F09E8	C;Genetics:
A;Gene: CESP:PF09BB.1	A;Map Position: 4	A;Intros: 18/1; 54/1; 97/1; 149/1
Query Match 25.0%; Score 5; DB 2; Length 240; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 15 LETKF 19 Db 89 LETKF 93	
RESULT 52		
3999833 hypothetical protein SA0589 [imported] - Staphylococcus aureus (strain N315) Species: Staphylococcus aureus Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2004 Accession: B89833 C.Species: Canis lupus familiaris (dog) C.Accession: A25296; A61227; A60142 C;Cross-references: UNIPROT:Q99VY2; GB:BA000018; PID:q13700524; PIDN:BAR41821..1; GSPDB:G A;Experimental source: strain N315 C;Genetics:		
A;Reference number: B89758; PMID:21311952; MUID:11418146 A;Accession: B89333 A;Status: Preliminary A;Molecule type: DNA A;Residues: 1-247 <KUR>		
Query Match 25.0%; Score 5; DB 2; Length 247; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 14 MLETK 18 Db 1 MLETK 5	
RESULT 53		
LNGPS		
Canis lupus familiaris (dog)		
N Alterate names: pulmonary surfactant 32k apoprotein; pulmonary surfactant-associated		
C.Species: Canis lupus familiaris (dog)		
C;Accession: A25296; A61227; A60142 R;Benson, B.; Hawgood, S.; Schilling, J.; Clements, J.; Damm, D.; Cordell, B.; White, R. Proc. Natl. Acad. Sci. U.S.A. 82, 6379-6383, 1985 A;Title: Structure of canine pulmonary surfactant apoprotein: cDNA and complete amino acid sequence A;Reference number: A25296; MUID:86016705; PMID:3863100 A;Accession: A25296 A;Molecule type: mRNA A;Residues: 1-248 <BEN>		
R;Note: the authors translated the codon TTG for residue 60 as Pro		
R;Liau, D.F.; Ryan, S.F.		
R;Chem. Phys. Lipids 59, 29-38, 1991		
A;Title: Purification of surfactant protein A from dog lung by reconstitution with surface		
A;Reference number: A61227; MUID:1790579		
A;Accession: A61227		
A;Molecule type: protein		
A;Residues: 18-32 <LIAs>		
R;Ross, G.P.; Meuth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A.		
R;Biogchem. Biophys. Acta 870, 267-278, 1986		
A;Title: Purification of canine surfactant-associated glycoproteins A. Identification of		

A;Residues: 1-250 <COL>
A;Cross-references: UNIPROT:053799; GB:AL021958; PIDN:CAA1750
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0736

Query Match Score 5; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LRCVC 12
Db 178 LRCVC 182

RESULT 56
S49055 - Streptomyces fradiae (strain T59235)
C;Species: Streptomyces fradiae
A;Variety: strain T59235
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 12-Jul-2004
C;Accession: S49055
R;Merton-Davies, J.A.; Cundliffe, E.
Mol; Microbiol. 13, 349-55, 1994
A;Title: Analysis of five tylosin biosynthetic genes from the tyIIBA region of the Strep
A;Reference number: S49051; MUID:95075319; PMID:7384112
A;Accession: S49055
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-253 <MER>
A;Cross-references: UNIPROT:Q54145; EMBL:U08223; PIDN:96849140; PIDN:AAA21345.1; PID:9473
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
C;Superfamily: type II thioesterase, NRPS/PKS/S-FAS type; oleoyl-lacyl-carrier-protein
F;16-232/Domain: oleoyl-lacyl-carrier-protein] hydrolase homology <ACP>>

Query Match Score 5; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MWLR 10
Db 1 MWLR 5

RESULT 57
G90275 hypothetical protein SSO1215 [Imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Accession: G90275
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char
Jong, I.; Jeffries, A.C.; Koerera, C.J.; Medina, N.; Peng, X.; Tri-NGOC, H.P.; Redder, P
Arettt, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90275
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <KUR>
A;Cross-references: UNIPROT:Q97YU2; GB:AE006641; NID:913814412; PIDN:AAK41462.1; GSPDB:G
C;Genetics:
A;Gene: SS01215

Query Match Score 5; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 WLRCV 11
Db 152 WLRCV 156

RESULT 58
C98274 nlp2 protein (AJ250581) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 12-Jul-2004
C;Accession: C98274
R;Goodner, B.; Hinkie, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C98274
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <KUR>
A;Cross-references: UNIPROT:Q8U9P1; GB:AE007870; PIDN:AAK89717.1; PID:915159631; GSPDB:G
C;Genetics:
A;Gene: AGR_L_2306
A;Map position: linear chromosome
C;Superfamily: type II thioesterase, NRPS/PKS/S-FAS type; oleoyl-lacyl-carrier-protein
Query Match Score 5; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGAPM 6
Db 3 RGAPM 7

RESULT 59
T29698 hypothetical protein F31A3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29698
R;Murray, J.; Le, T.T.
A;Description: The sequence of C. elegans cosmid F31A3.
A;Reference number: Z200667
A;Accession: T29698
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-262 <MTR>
A;Cross-references: UNIPROT:Q19918; EMBL:U58742; PIDN:AAB36855.1; GSPDB:GN00028; CESP:F31A3
C;Genetics:
A;Gene: CEP:F31A3.2
A;Map position: X
A;Introns: 23/3; 80/2; 155/2
Query Match Score 5; DB 2; Length 252;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETKF 19
Db 97 LETKF 101

RESULT 60
H83956 flagellar assembly protein flh [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83956
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83956
A;Status: preliminary
A;Molecule type: DNA

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>A;Residues: 1-266 <STO>
>A;Cross-references: UNIPROT:Q9KA34; GB:AP001515; GB:BA000004; NID:910174886; PIDN:BA0061
>A;Experimental source: strain C-125
>C;Genetics:
>A;Gene: flhH

Query Match      25.0%; Score 5; DB 2; Length 266;
Best Local Similarity 100.0%; Prd. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   15 LETKF 19
      |||||
Db    233 LETKF 237

RESULT 61
T00114
exodeoxyribonuclease III (EC 3.1.11.2) - Actinobacillus actinomycetemcomitans
>C;Species: Actinobacillus actinomycetemcomitans
>C;Date: 22-Jun-1999 #sequence_revision 22-Jun-1999 #text_change 09-Jul-2004
>C;Accession: T00114
>A;Title: A gene cluster for 6-deoxy-L-talose synthesis in Actinobacillus actinomycetemcomitans
>A;Biobium: Biobium, Acta 1442, 409-414, 1998
>A;Reference number: Z14111; MUID:99023768; PMID:9805002
>A;Accession: T00114
>A;Status: translated from GB/EMBL/DDJB
>A;Molecule type: DNA
>A;Residues: 1-267 <NAK>
>A;Cross-references: UNIPROT:O66261; EMBL:AB010415; NID:91132248; PIDN:BAA28143.1; PID:93
>A;Experimental source: strain NCTC 9710
>C;Function:
>A;Description: catalyzes degradation of double-stranded DNA; removes damaged DNA at cyto
  tion
>C;Superfamily: exodeoxyribonuclease III
>C;Keywords: DNA repair; hydrolase

Query Match      25.0%; Score 5; DB 2; Length 267;
Best Local Similarity 100.0%; Prd. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   15 LETKF 19
      |||||
Db    96 LETKF 100

RESULT 62
T21429
hypothetical protein F26H11.5 - Caenorhabditis elegans
>C;Species: Caenorhabditis elegans
>C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
>C;Accession: T21429
>A;Reference number: Z19421
>A;Accession: T21429
>A;Status: preliminary; translated from GB/EMBL/DDJB
>A;Molecule type: DNA
>A;Residues: 1-273 <WIL>
>A;Cross-references: EMBL:Z81515; PIDN:CA04193.1; GSPDB:GN000020; CESPP:F26H11.5
>A;Experimental source: clone F26H11.1
>C;Genetics:
>A;Gene: CESPP:F26H11.5
>A;Map position: 2
>A;Introns: 5/3; 159/3

Query Match      25.0%; Score 5; DB 2; Length 273;
Best Local Similarity 100.0%; Prd. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   16 ETIKF 20
      |||||

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C;Accession: T27610
R;Du, Z.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of *C. elegans* cosmid ZC477.
A;Accession: Z20392
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Cross-references: EMBL:U40802; PIDN:AAA81511.1; CESP:ZC477.8
C;Genetics:
A;Gene: CESP:ZC477.8
A;Introns: 7/7
Query Match 25.0%; Score 5; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 13 QMLET 17
Db 180 QMLET 184

RESULT 68
T24827
hypothetical protein T11B7.3 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Gardner, A.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z19940
A;Accession: T24827
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-296 <WIL>
A;Cross-references: UNIPROT:Q22389; EMBL:Z54237; PIDN:CAA90989.1; GSPDB:GN00022; CESP:T11B7.3
C;Genetics:
A;Gene: CESP:T11B7.3
A;Map Position: 4
A;Introns: 45/3; 111/1; 270/1
Query Match 25.0%; Score 5; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PRGAP 5
Db 112 PRGAP 116

RESULT 69
E70745
hypothetical protein Rv0498 - *Mycobacterium tuberculosis* (strain H37RV)
C;Species: *Mycobacterium tuberculosis*
C;Accession: E70745
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70745
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-280 <COL>
A;Cross-references: UNIPROT:Q11163; GB:Z77162; GB:AI123456; PIDN:CAB00924.
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv0498
C;Superfamily: Streptomyces coelicolor hypothetical protein SCE7.14c
Query Match 25.0%; Score 5; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 VCQML 15
Db 235 VCQML 23/9

RESULT 67
T22501
hypothetical Protein F52D10.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Accession: T22501
R;Kershaw, J.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z19571
A;Accession: T22501
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-284 <WIL>
A;Cross-references: UNIPROT:Q20656; EMBL:Z66564; PIDN:CAA91475.1; GSPDB:GN00028; CESP:F52D10.4
A;Experimental source: clone F52D10
C;Genetics:
A;Gene: CESP:F52D10.4
A;Map position: X

RESULT 70
T20906
hypothetical protein F14F7.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T20906
 R;McMurray, A.
 Submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19345
 A;Accession: T20906
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-305 <WLI>
 A;Cross-references: UNIPROT:O17805; EMBL:Z81503; PIDN:CARB04111.1; GSPDB:GN00021; CESP:FI
 C;Genetics:
 A;Gene: CESP-F14F7.1
 A;Map position: 3
 A;Introns: 27/3; 49/3
 Query Match Score 5; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 PRGAP 5
 Db 193 PRGAP 197

RESULT 71
 AD2202 transcription regulator all3171 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004,
 C;Accession: AB2202
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Saamoto, S.; Watanabe, A.; Iriuchii
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A;Reference number: AB1807; MUID:21595285; PMID:11759810
 A;Accession: AB2202
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-306 <KUR>
 A;Cross-references: UNIPROT:QBYSB8; GB:BA000019; PIDN:BAB74870.1; PID:917132266; GSPDB:G
 C;Genetics:
 A;Gene: all3171

Query Match Score 5; DB 2; Length 306;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 16 ETKFL 20
 Db 107 ETKFL 111

RESULT 72
 H75019 hypothetical protein PAB1459 - Pyrococcus abyssi (strain Orsay)
 C;Species: Pyrococcus abyssi
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999
 A;Reference number: A75001
 A;Accession: H75049
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <WLI>
 A;Cross-references: UNIPROT:Q9T9W9; GB:AJ248287; GB:AL096836; NID:95458657; PIDN:CAB5029
 C;Genetics:
 A;Gene: PAB1459

C;Superfamily: Pyrococcus abyssi hypothetical protein PAB1459
 C;Accession: T20906
 R;McMurray, A.
 Submitted to the EMBL Data Library, November 1996
 A;Reference number: Z19345
 A;Accession: T20906
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-305 <WLI>
 A;Cross-references: UNIPROT:O17805; EMBL:Z81503; PIDN:CARB04111.1; GSPDB:GN00021; CESP:FI
 C;Genetics:
 A;Gene: CESP-F14F7.1
 A;Map position: 3
 A;Introns: 27/3; 49/3
 Query Match Score 5; DB 2; Length 306;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 2 RGAPM 6
 Db 181 RGAPM 185

RESULT 73
 GT1110 hypothetical protein PH0654 - Pyrococcus horikoshii
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C;Accession: GT1110
 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Hino, Y.; Yamamoto, S.; Sekine
 M.M.; Ohfuki, Y.; Funahashi, T.; Tanaka, T.; Kudon, Y.; Yamazaki, J.; Kishida, N.; Oguchi,
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues 1-308 <WLI>
 A;Cross-references: UNIPROT:O5838B; GB:AP000003; NID:93236130; PID:9329745.1; PID:9325.
 A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH0654

Query Match Score 5; DB 2; Length 308;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 2 RGAPM 6
 Db 181 RGAPM 185

RESULT 74
 T49591 probable 35 kDa ribonuclease H [imported] - Neurospora crassa
 C;Species: Neurospora crassa
 C;Accession: T49591
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 A;Submitted to the Protein Sequence Database, May 2000
 A;Reference number: Z25022
 A;Accession: T49591
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-117 <SCH>
 A;Cross-references: UNIPROT:Q9P5X8; EMBL:AL355931; GSPDB:GN00116; NCSP: B3E4.40
 C;Genetics:
 A;Gene: NCSP:B3E4.40
 A;Accession: H75049
 A;Map position: 6
 A;Introns: 223/1

Query Match Score 5; DB 2; Length 317;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 14 MLETK 18
 Db 264 MLETK 268

RESULT 75
 T333845

hypothetical protein Y44E3A.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33845
R;Woessner, J.; Graves, T.; Keppeler, D.
submitted to the EMBL Data Library, November 1998
A;Description: The sequence of C. elegans cosmid Y44E3A.
A;Reference number: Z21422
A;Accession: T33845
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-318 <WOE>
A;Cross-references: UNIPROT:Q9TZX0; EMBL:AF106589; PIDN: AAC78231.1; GSPDB:GN00019; CESP:
C;Experimental source: strain Bristol N2; clone Y44E3A
C;Genetics:
A;Gene: CESP:Y44E3A.5
A;Map position: 1
A;Introns: 6/3; 41/1; 155/3; 223/3
Query Match Score 5; DB 2; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.8e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 LETKF 19
| | | |
Db 167 LETKF 171

Search completed: October 26, 2004, 07:23:39
Job time : 19.5 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	7	35.0	82	087JN1	Q8vjin1 mycobacteri
2	6	30.0	179	1 TNN9_BOVIN	Q8tb83 bos taurus
3	6	30.0	188	2 Q8FB70	Q8tb70 homo sapien
4	6	30.0	211	2 Q87727	Q87727 vibrio algi
5	5	30.0	224	2 QFZC2	Q0ezcz staphylococ
6	6	30.0	226	1 TNN9_HUMAN	Q14530 homo sapien
7	6	30.0	226	1 TNN9_MOUSE	Q9cq79 mus musculus
8	8	30.0	226	1 TNN9_RAT	Q8k581 rattus norvegicus
9	6	30.0	226	2 CG43216	Cag33216 homo sapi
10	6	30.0	238	2 P73223	P73223 synechocyst
11	6	30.0	250	2 QP4ZB	Q7p4z8 fusobacteri
12	6	30.0	253	2 QHK94	Q6hk94 bacillus th
13	6	30.0	253	2 Q73A41	Q73a41 bacillus ce
14	6	30.0	253	2 Q81S20	Q81s20 bacillus an
15	6	30.0	253	2 AAS40868	Aas40868 bacillus an
16	6	30.0	253	2 ART30974	Aat3074 bacillus ha
17	6	30.0	259	2 QFP9X7	Q6p9x7 rattus norvegicus
18	6	30.0	259	2 AAH60541	Aah60541 rattus no
19	6	30.0	267	2 AAH70183	Aah70183 homo sapi
20	6	30.0	271	1 AROE_CLOSE	Q8xmi8 clostridium
21	6	30.0	278	1 AROE_BACHD	Q9kd93 bacillus ha
22	6	30.0	315	2 QVLD6	Q9vld6 drosophila
23	6	30.0	319	2 Q810R3	Q8ior3 drosophila
24	6	30.0	384	2 Q9C280	Q9c280 neurospora
25	6	30.0	388	2 Q6P387	Q6p387 homo sapien
26	6	30.0	388	2 AAH64143	Aah64143 homo sapi
27	6	30.0	395	2 Q96MA7	Q96ma7 homo sapien
28	6	30.0	421	1 RSMB_XTLFA	Q9perv xylylla fass
29	6	30.0	426	1 RSMB_VIBVU	Q8ddes vibrio vuln
30	6	30.0	426	1 RSMB_VIBVY	Q7mgk vibrio vuln
31	6	30.0	427	1 RSMB_VIBPA	Q87tk3 vibrio para

RESULT 1							
Q8VJN1	PRELIMINARY;	PRT;	82 AA.				
ID							
AC							
DT	01-MAR-2002 (TREMBLrel. 20, Created)						
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)						
DB	Hypothetical protein MT2341.						
GN	OrderedLocusNames=MT2341;						
OS	Mycobacterium tuberculosis.						
OC	Actinobacteria; Actinomycetales;						
OC	Corynebacteriales; Mycobacteriaceae; Mycobacterium.						
OX	NCBI_TaxID:1773;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAN=CDC / 1551 / Oshkosh.						
RX	MEDLINE=22206434; PubMed=12218036;						
RA	Fleischmann R.D., Allard D., Eisen J.A., Carpenter L., White O.,						
RA	Peterson J.D., DeBoy R.J., Nelson D., Haft D.H., Gwinn M.L., Utterback T.R., Weidman J.F., Khouri H.M., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.; RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and RT Laboratory strains"; DR EMBL; AE007077; AAK46625.1; -.						
DR	TIGR; MT2341; -.						
KW	Hypothetical protein.						
SQ	SEQUENCE 82 AA; 8995 MW; C46009PE4E66DC09E CRC64;						
Query Match	35.0%; Score 7; DB 2; Length 82;						
Best Local Similarity	100.0%; Pred. No. 3.1;						
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	2 RGAPMNL 8						
Db	6 RGAPMNL 12						
RESULT 2							
TXN9_BOVIN	STANDARD;	PRT;	179 AA.				
ID	01883; TXN9_BOVIN						
AC	01883;						
DT	15-JUL-1999 (Rel. 3B, Created)						
DT	15-JUL-1999 (Rel. 3B, Last sequence update)						
DT	01-OCT-2004 (Rel. 45, Last annotation update)						
DE	Hypothodoxin domain containing protein 9 (Protein 1-4) (Fragment).						
GN	Name=TXNDC9; Synonyms=APACD;						
OS	Bos taurus (Bovine).						
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.						
OC	NCBI_TaxID:9913;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE-Bone marrow;						
RA	Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.						
RA	Brule S., Lusier J.G.; "Bovine ATP binding protein." ; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.						
RA	"-SIMILARITY: Belongs to the UPF0011 family. Some similarity to the thioredoxin family.						
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CC	EMBL; AF027733; AAB84006.1; -.						
DR	InterPro; IPR006662; Thioredoxin.						
DR	InterPro; IPR066663; Thioredoxin_1.						
DR	Pfam; PF00085; Thioredoxin.						
FT	NON_TER	1	1				
SQ	SEQUENCE 179 AA; 21051 MW; 6873189499AD494 CRC64;						
Query Match	30.0%; Score 6; DB 1; Length 179;						
Best Local Similarity	100.0%; Pred. No. 79;						
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	15 LETKFL 20						
Db	49 LETKFL 54						
RESULT 3							
Q8TB70	PRELIMINARY;	PRT;	188 AA.				
ID	Q8TB70						
AC	Q8TB70;						
DT	01-JUN-2002 (TREMBLrel. 21, Created)						
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)						
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)						
DR	APACD protein.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.						
OC	NCBI_TaxID:9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE-Bone marrow;						
RX	MEDLINE=22388257; PubMed=12477932;						
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schulter G.D., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Zeeberg B.B., Butow K.H., Schaeffer C.F., Bhat N.K., Altenschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J., Bosak S.A., McEvran K.J., Malek J.A., Grunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schein J.B., Jones S.J., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).						
RN	[2]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE-Bone marrow;						
RA	Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.						
DR	GO; GO:0005439; FE:electron transporter activity; IEA.						
DR	GO; GO:0006118; FE:electron transporter activity; IEA.						
DR	InterPro; IPR066662; Thioredoxin.						
DR	InterPro; IPR06663; Thioredoxin_1.						
DR	Pfam; PF00085; Thioredoxin.						
KW	Redox-active center.						
RN	SEQUENCE FROM N.A.						
RC	TISSUE-Bone marrow;						
RA	Strausberg R.; BC024223; AAH24223.2; -.						
DR	GO; GO:0005439; FE:electron transporter activity; IEA.						
DR	GO; GO:0006118; FE:electron transporter activity; IEA.						
DR	InterPro; IPR06662; Thioredoxin.						
DR	InterPro; IPR06663; Thioredoxin_1.						
DR	Pfam; PF00085; Thioredoxin.						
KW	SEQUENCE 188 AA; 22199 MW; B375C22B62DF6523 CRC64;						
Query Match	30.0%; Score 6; DB 2; Length 188;						
Best Local Similarity	100.0%; Pred. No. 82;						
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	15 LETKFL 20						
Db	119 LETKFL 124						

RESULT 4
O87727 PRELIMINARY; PRT; 211 AA.

AC Q87727; PRELIMINARY; PRT; 211 AA.
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fmu protein.
GN Name=Fmu;
OS Vibrio alginolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibriionaceae; Vibrio.
OX NCBI_TaxID=663;
RN [1] _
RP SEQUENCE FROM N.A.
RC STRAIN=138-2;
RX MEDLINE=93386520; PubMed=9720051;

RA Nakamura T., Yamamoto N., Stumpf S., Uemoto T., Bakker E.P.;
RT "Cloning of the trkAH gene cluster and characterization of the Trk K+ -
RT uptake system of Vibrio alginolyticus.";
RL Microbiology 144: 2281-2289(1998).
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0006355: P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001678; Fmu_N01/Nop2p.
DR InterPro; IPR006027; NusB.
DR InterPro; IPR006174; NusB region.
DR Pfam; PF01199; N01; Nop2_Fmu; 1.
DR ProDom; PRO005242; NusB region; 1.
SQ SEQUENCE 211 AA; 24135 MW;

Query Match 30.0%; Score 6; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 APMWLR 9
Db 169 APMWLR 174

RESULT 5
Q9EZC2 PRELIMINARY; PRT; 224 AA.

AC Q9EZC2; PRELIMINARY; PRT; 224 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IS1182 transposase.
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
OX NCBI_TaxID=1285;
RN [1] _
RP SEQUENCE FROM N.A.

RC STRAIN=MIS-2;
RX MEDLINE=21154722; PubMed=11230937;
RA Boerlin P., Burns A.P., Frey J., Kuhnert P., Niclouet J.;
RT "Molecular epidemiology and genetic linkage of macrolide and
RT aminoglycoside resistance in Staphylococcus intermedius of canine
RT origin.";
RL Vet Microbiol. 79:155-169 (2001).
DR EMBL; AF290292; AAG2229.; -;
SQ SEQUENCE 224 AA; 26309 MW; COE3400DDC9B8F1D CRC64;

Query Match 30.0%; Score 6; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 QMLETK 18
Db 174 QMLETK 179

RESULT 6
TXN9 HUMAN STANDARD; PRT; 226 AA.
ID TXN9_HUMAN STANDARD; PRT; 226 AA.
AC O14510; QENSFS; Q9BRU6; Created
DT 15-JUL-1993 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Thioredoxin domain containing protein 9 (Protein 1-4) (ATP binding
DE protein associated with cell differentiation).
DE Name=TXN9; Synonyms=APC4D;
GS Homo sapiens (Human).
GO Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1] _
RN SEQUENCE FROM N.A.
RP TISSUE=Leukemia;
RC TISSUE=Bone marrow, Brain, and Kidney;
RA Shiosaka T.;
RA "Differential expression of 1-4 gene in functionally distinct MB-1
RT subclones";
RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN [2] _
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schattner R., Henze S., Korn B.;
RA "Cloning of human full open reading frames in Gateway(TM) system entry
RT vector (pDONR201).";
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN [3] _
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow, Brain, and Kidney;
RX MEDLINE=242603899; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grusec L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schueler G.D.,
RA Altschul S.F., Zeeberg B.R., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsisna K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schaetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahay S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC |- FUNCTION: Not known, associated with cell differentiation.
CC |- SIMILARITY: Belongs to the UPF0071 family. Some similarity to the
CC thioredoxin family.

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DR EMBL; AB006679; BA21281.1; -;
DR EMBL; CR456935; CAG33216.1; -;
DR EMBL; BC005968; AAH05968.1; -;
DR EMBL; BC022864; AAH22864.1; -;
DR EMBL; BC070183; AAH70183.1; ALT_INIT.
DR Genew; HGNC:24110; TXNDC5.
DR InterPro; IPR006662; Thioredoxin.
DR InterPro; IPR016663; Thioredoxin_dom2.
DR Pfam; PF00085; Thioredoxin_1.

FT	CONFLICT	122	122	K -> N (in Ref. 1).	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Faby J., Helton E., Kenteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiteley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smailus D.E., Scheiner A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human RT	
FT	SEQUENCE	214	214	I -> M (in Ref. 1).	RA	RT and mouse cDNA sequences.";	
SQ	SEQUENCE	226 AA;	26534 MW;	2735A256D114C3 CRC64;	RA	RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
Query Match	Best Local Similarity	30.0 %;	Score 6;	DB 1;	Length 226;	RL	-!- FUNCTION: Not known, associated with cell differentiation (By CC
	Matches 6;	Conservative 0;	Pred. No. 97;	Indels 0;	Gaps 0;	CC	-!- SIMILARITY: Belongs to the UPE0071 family. Some similarity to the CC thioredoxin family.
QY	15 LETKFL 20					CC	-!- SIMILARITY: Belongs to the UPE0071 family. Some similarity to the CC thioredoxin family.
Db	119 LETKFL 124					CC	-!- SIMILARITY: Belongs to the UPE0071 family. Some similarity to the CC thioredoxin family.
<hr/>							
RESULT 7							
ID	TXN9_MOUSE	STANDARD;	PRT;	226 AA.	DR	EMBL; AK002893; BAB22438.1;	
AC	Q9CQ79				DR	EMBL; AK006170; BAB22440.1;	
DT	01-OCT-2004	(Rel. 45, Created)			DR	EMBL; AK010709; BAB227134.1;	
DT	01-OCT-2004	(Rel. 45, Last sequence update)			DR	EMBL; AK011424; BAB22761.1;	
DT	01-OCT-2004	(Rel. 45, Last annotation update)			DR	EMBL; AK016756; BAB30412.1;	
DE	Thioredoxin domain containing protein 9 (ATP binding protein DE associated with cell differentiation).				DR	EMBL; AK028525; BAC25991.1;	
GN	Name=txndc9; Synonyms=Apccd9;				DR	EMBL; BC022947.1; AAH22947.1;	
OS	Mus musculus (Mouse);				DR	MGI: 2138153; Apacd9.	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Mus.				DR	Intero protein IPR006662; Thioredoxin.	
OX	NCBI TaxID:10050;				DR	InterPro: IPR006663; Thioredoxin_dom2.	
RN	[1]				DR	Pfam: PF00085; Thioredoxin_1.	
RP	SEQUENCE FROM N.A.				DR	SEQUENCE 226 AA; B90255DDAEE402BC CRC64;	
RC	STRAIN=C57BL/6J;				DR	Query Match 30.0%; Score 6; DB 1; Length 226;	
RC	TISSUE=Embryo; Embryonic stem cells, Kidney, Skin, and Testis;				DR	Best Local Similarity 100.0%; Pred. No. 97;	
RC	MEDLINE=21354683; PubMed=12466051; DOI=10.1038/nature01266;				DR	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaiko I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer C.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimm S., Guistinovich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanaai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Numata K., Okido T., Pavan W.J., Perera G., Pesole G., Pavasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultan A., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishizawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashimoto W., Inotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y., RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";	DR	RESULT 8 TXN9_RAT STANDARD; PRT; 226 AA.				
RA	Nature 420:563-573 (2002).				DR	SEQUENCE FROM N.A.	
RN	[2]				DR	Li Y., Xu C., Zhang Y.;	
RP	SEQUENCE FROM N.A.				DR	"Cloning and analysis of up-regulated genes in rat liver."	
RX	MEDLINE=223825; PubMed=12477932; DOI=10.1073/pnas.242603899;				DR	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Klausner S.P., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	DT	-!- FUNCTION: Not known, associated with cell differentiation (By CC				
RA	RT				DT	-!- SIMILARITY: Belongs to the UPE0071 family. Some similarity to the CC thioredoxin family.	
<hr/>							
RESULT 8							
ID	TXN9_RAT				AC	Q9K8L1;	
DT	01-OCT-2004 (Rel. 45, Created)				DT	01-OCT-2004 (Rel. 45, Last sequence update)	
DE	Thioredoxin domain containing protein 9 (ES cell-related protein).				DT	01-OCT-2004 (Rel. 45, Last annotation update)	
GN	Name=txndc9;				DT	OS Ratetus norvegicus (Rat).	
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				DR	OC NCBI TaxID-10016;	
RN	[1]				DR	NCBI TaxID-10116;	
RP	SEQUENCE FROM N.A.				DR	RP SEQUENCE FROM N.A.	
RA	Li Y., Xu C., Zhang Y.;				RA	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way	
RA	"Cloning and analysis of up-regulated genes in rat liver."				RA	use by non-profit institutions as long as its content is in no way	
RA	Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.				RA	use by non-profit institutions as long as its content is in no way	
RA	-!- FUNCTION: Not known, associated with cell differentiation (By CC				RA	use by non-profit institutions as long as its content is in no way	
RA	-!- SIMILARITY: Belongs to the UPE0071 family. Some similarity to the CC thioredoxin family.				RA	use by non-profit institutions as long as its content is in no way	

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC DR EMBL; AF508022; AAM34684.1; ALT INIT.
 DR InterPro; IPR006653; Thiorodox dom2.
 SQ SEQUENCE 226 AA; 26272 MW; EDAS5BP54C18AE68A CRC64;

Query Match 30.0%; Score 6; DB 1; Length 226;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 15 LETKFL 20
 Db 119 LETKFL 124

RESULT 9
 ID CAG33216 PRELIMINARY;
 AC CAG33216; PRT; 226 AA.
 DR 01-JUN-2004 (TREMBLrel. 27; Created)
 DT 01-JUN-2004 (TREMBLrel. 27; Last sequence update)
 DT 01-JUN-2004 (TREMBLrel. 27; Last annotation update)
 DE APACD protein.
 GN APACD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert L., Schick M., Neubert P., Schatten R., Korn B.;
 RT "Cloning of human full open reading frames in Gateway (TM) system entry
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR456335; CAG33216.1; -.
 SQ SEQUENCE 226 AA; 26534 MW; 2735AA2562D1143C3 CRC64;

Query Match 30.0%; Score 6; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 15 LETKFL 20
 Db 119 LETKFL 124

RESULT 10
 ID P73223 PRELIMINARY;
 AC P73223; PRT; 238 AA.
 DR 01-FEB-1997 (TREMBLrel. 02; Created)
 DT 01-FEB-1997 (TREMBLrel. 02; Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
 DE SII1925 protein.
 GN OrderedLocusNames=sII1925;
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TAXID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugiyama M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 648 to 928 of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE=97061201; PubMed=8905231;

RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Sugiyama M., Sasaki T., Kimura T.,
 RA Hosouchi T., Hino M., Matsuno A., Muraki A., Nakazaki N., Narita K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watabane A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:1:09-136(1996).
 DR EMBL; D90904; BX117250.1; -.
 DR S75336; S75336.
 KW Complete proteome.
 SQ SEQUENCE 238 AA; 25843 MW; F016A42E3DD3E588 CRC64;
 Query Match 30.0%; Score 6; DB 2; Length 238;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 15 LETKFL 20
 Db 165 LETKFL 170

RESULT 11
 ID QTP4Z8 PRELIMINARY;
 AC QTP4Z8; PRT; 250 AA.
 DR 01-MAR-2004 (TREMBLrel. 26; Created)
 DT 01-MAR-2004 (TREMBLrel. 26; Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26; Last annotation update)
 DE Shikimate 5-dehydrogenase (EC 1.1.1.25).
 Name=FAV0648;
 OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium.
 RN [1] CAUTION: The sequence shown here is derived from an
 NCBI_TAXID=209892;
 RN SEQUENCE FROM N.A.
 RC STRAIN=ATCC 49256.
 RA Karpatra V., Ivanova N., Anderson L., Reznik G., Bhattacharyya A.,
 RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
 RA Haselkorn R., Overbeek R., Kyrides N.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases
 -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABF0100090; BAA23737.1; -.
 DR GO; GO:0005137; C:cytoplasm; IBA.
 DR GO; GO:0016491; F:oxidoreductase activity; IBA.
 DR GO; GO:004764; F:shikimate 5-dehydrogenase activity; IBA.
 DR InterPro: IPR001151; Shikimate DH.
 DR Pfam; PF01488; Shikimate_DH; 1.
 KW Oxidoreductase.
 SQ SEQUENCE 250 AA; 28872 MW; 7FFF3D1EE8750DDA CRC64;
 Query Match 30.0%; Score 6; DB 2; Length 250;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;

Qy 15 LETKFL 20
 Db 187 LETKFL 192

RESULT 12
 ID Q6HK94 PRELIMINARY;
 AC Q6HK94; PRT; 253 AA.
 DR 05-JUL-2004 (TREMBLrel. 27; Created)
 DT 05-JUL-2004 (TREMBLrel. 27; Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27; Last annotation update)
 DE Hypothetical protein.

OS	Bacillus anthracis.
OS	Bacillus thuringiensis serovar konkukian str. 97-27.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC	Bacillus thuringiensis serovar konkukian.
OX	NCBI_TaxID=281309;
[1]	SEQUENCE FROM N.A.
RN	
RP	SEQUENCE FROM N.A.
RC	STRAIN=97-27;
RC	BRUCE D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA	Pettinelli H., Tournasse N.J., Baillie L.W., Paulsen I.T.,
RA	Read T.D., Nelson K.E., Eisen J.A., Gill S.R.,
RA	Holtzapfel E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA	Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA	DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA	Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA	Bentton J.L., Mahamoud Y., Jiang L., Hance J.R., Weidman J.F.,
RA	Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Newman W.C.,
RA	Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA	Salzberg S.L., Thomason B., Koehler T.M.,
RA	Hanna P.C., Kolstoe A.-B., Fraser C.M.,
RA	"the genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria.";
RT	RT
RT	"the genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria.";
RL	Nature 423:81-86 (2003).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RA	Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B., Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L., Fraser C.M.;
RA	" <i>Bacillus anthracis</i> comparative genomics".
RA	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RL	[3]
RN	SEQUENCE FROM N.A.
RC	SEQUENCE FROM N.A.
RA	Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H., Subtil (JAN-2004) to the EMBL/GenBank/DBJ databases.
RA	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RI	AB017030; AAP25762.1; -.
DR	AEO17334; AAT30974.1; -.
DR	AEO17225; AAT54039.1; -.
DR	TIGR; BA1859; -.
DR	GO:0016491; FAD-oxidoreductase activity; IBA.
DR	GO:0006735; Pararomatic compound metabolism; IBA.
DR	GO:0006118; P-selectin transport; IBA.
DR	InterPro; IPR04183; LigB.
DR	PFAM; PF02900; LigB; 1.
SQ	SEQUENCE 253 AA; 28193 MW;
SQ	863533F0058A872E CRC64;
Qy	Query Match 30.0%; Score 6; DB 2; Length 253;
Db	Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 MLETKF 19
Db	87 MLETKF 92
[1]	SEQUENCE FROM N.A.
AC	Q73A41; PRELIMINARY;
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusName=BCE1944;
GN	Bacillus cereus (strain ATCC 10987).
OS	Bacterium; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC	
OX	NCBI_TaxID=222523;
RN	
RP	SEQUENCE FROM N.A.
RC	PubMed:14960714;
RA	Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tournasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RA	"The genome sequence of <i>Bacillus cereus</i> ATCC 10987 reveals metabolic adaptations and a large plasmid related to <i>Bacillus anthracis</i> pXO1.";
RT	RT
RT	Nucleic Acids Res. 32:977-988 (2004).
RL	DR
DR	EMBL; AE017270; AAS40868.1; -.
DR	TIGR; BCE1944; -.
DR	InterPro; IPR004183; LigB.
DR	PFAM; PF02900; LigB; 1.
DR	Complete proteome.
DR	SEQUENCE 253 AA; 28543 MW;
DR	C36AC1D894E451BA CRC64;
Qy	Query Match 30.0%; Score 6; DB 2; Length 253;
Db	Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	14 MLETKF 19
Db	87 MLETKF 92
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 24, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	02-MAR-2004 (TREMBLrel. 27, Created)
DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT	04-MAY-2004 (TREMBLrel. 27, Last annotation update)
DE	Oxidoreductase.
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	02-MAR-2004 (TREMBLrel. 27, Created)
DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT	04-MAY-2004 (TREMBLrel. 27, Last annotation update)
DE	Oxidoreductase.
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
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OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
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DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
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OS	Bacillus cereus (strain ATCC 10987).
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NCBI_TaxID=222523;	
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AC	Q81S20; Q610A0; Q6KU74;
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AC	Q81S20; Q610A0; Q6KU74;
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[1]	SEQUENCE FROM N.A.
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AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
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NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
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AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
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GN	BCE1944.
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NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
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GN	BCE1944.
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NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10987).
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=222523;	
[1]	SEQUENCE FROM N.A.
AC	Q81S20; PRELIMINARY;
AC	Q81S20; Q610A0; Q6KU74;
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE	Oxidoreductase.
DN	OrderedLocusNames=BA1859; BAS1723; ORFNNames=GBAA1859;
GN	BCE1944.
OS	Bacillus cereus (strain ATCC 10

- Nucleic Acids Res. 28:4317-4331(2000).
CC -1- CATALYTIC ACTIVITY; Shikimate + NADP(+) = 5-dehydroshikimate + NADPH.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
CC fourth step.
CC -1- SIMILARITY: Belongs to the shikimate dehydrogenase family.
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CC DR EMBL; AP001511; BAB05043.1; -.
DR PIR; D83815; D83815.
DR HSSP; Q58484; INVT.
DR HAMAP; MF_00022; -; 1.
DR InterPro; IPR006151; Shikimate DH.
DR Pfam; PF01488; Shikimate DH; 1.
DR TIGRFAMS; TIGR0050; aroE; 1.
DR TIGRFAMS; TIGR1809; Shikimate-DH-AROM; 1.
KW Aromatic amino acid biosynthesis; Complete proteome; NADP; KW Oxidoreductase; SEQUENCE 278 AA; 30630 MW; 2000144C84686264 CRC64;
SQ Query Match 30.0%; Score 6; DB 1; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
[3]
Qy 15 LETKF1 20
Db ||||| 230
Db RESULT 22
ID Q9VLD6 PRELIMINARY; PRT; 315 AA.
AC Q9VLD6;
DT 01-MAY-2000 (TREMBLref); 13, Created)
DT 01-MAY-2000 (TREMBLref); 13, Last sequence update)
DT 05-JUL-2004 (TREMBLref); 27, Last annotation update)
GN CG4454-PA (LID36125p).
ORFNames=CG4454;
OS Drosophila melanogaster (Fruit fly).
Drosophila melanogaster; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
NCBI_TAXID=7227;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D.; Celiker S.E.; Holt R.A.; Evans C.A.; Gocayne J.D.; Amanatides P.G.; Scherer S...; Li P.W.; Hoskins R.A.; Galle R.F.' George R.A.; Lewis S.E.; Richards S.; Ashburner M.; Henderson S.N.; Sutton G.G.; Wortman J.R.; Yandell M.D.; Zhang Q.; Chen L.X.; Brandon R.C.; Rogers Y.H.; Ilavitz R.G.; Champe M.; Pfeiffer B.D.; Wan H.; Doyle C.; Baxter G.C.; Heit G.; Neilson C.R.; Gabor G.L.; Abril J.F.; Agbayani A.; An H.J.; Andrews-Pfannkoch C.; Baldwin D.; Ballieu R.M.; Basu A.; Baxendale J.; Bayraktaroglu L.; Beasley E.M.; Beeson K.Y.; Benos P.V.; Berman B.P.; Bhandaari D.; Bolshakov S.; Borckova D.; Botchan M.R.; Bouck J.; Brokstein P.; Brottaker P.; Burtis K.C.; Busam D.A.; Butler H.; Cadieu E.; Center A.; Chandra I.; Cherry J.M.; Cawley S.; Dahlke C.; Davenport L.B.; Davies P.; de Pablo B.; Delcher A.; Deng J.; Dietz S.M.; Dodson K.; Doup L.B.; Downes M.; Dujan-Rocha S.; Dunkov B.C.; Dunn P.; Durbin K.J.; Evangelista C.C.; Ferraz C.; Ferriera S.; Fleischmann W.; Fosler C.; Gabrielian A.E.; Garg N.S.; Gelbart W.M.; Glasser K.; Glodek A.; Gong F.; Gorrell J.H.; Gu Z.; Guan P.; Harris M.; Harris N.L.; Harvey D.; Heiman T.J.; Herranz J.R.; Honck J.; Hostin D.; Housseron K.A.; Howland T.J.; Wei M.H.; Ikegami C.; Jalali M.; Kalush F.; Karpen G.H.; Ke Z.; Kennison J.A.; Ketchum K.A.; Kimmel B.E.; Kodira C.D.; Kraft C.; Kravitz S.; Kulp D.; Lai Z.; Lasko P.; Lei Y.; Levitsky A.A.; Li J.; Li Z.; Liang Y.; Lin X.; Liu X.; Mattei B.; McIntosh T.C.; McLeod M.P.; Morris J.C.; Merkulov G.; Milashina N.V.; Mobarry C.; Morris D.; Mount S.M.; Moy M.; Murphy B.; Murphy L.; Muzny D.M.; Nelson D.L.; Palazzolo M.; Pettman G.S.; Pan S.; Pollard J.; Purji V.; Reese M.G.; Reinert K.; Remington K.; Saunders R.D.; Scheeler F.; Shen H.; Shu B.C.; Siden-Kiamos I.; Simpson M.; Skupski M.P.; Smith T.; Spier B.; Spradling A.C.; Stapleton M.; Strong R.; Sun E.; Svärskas R.; Tector C.; Turner R.; Venter E.; Wang A.H.; Wang X.; Wang Z.Y.; Wasserman D.A.; Weinstock G.M.; Weissbach H.; Williams S.M.; Woodger, Worley K.C.; Wu D.; Yang S.; Yao Q.A.; Ye J.; Yeh R.F.; Zaveri J.S.; Zhan M.; Zhang G.; Zhao Q.; Zheng L.; Zheng X.H.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.; Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.; DR "The genome sequence of *Drosophila melanogaster*"; RT Science 287:2185-2195 (2000).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celinker S.E.; Wheeler D.A.; Kronmiller B.; Carlson J.W.; Haibern A.; Patel S.; Adams M.; Champe M.; Dugan S.P.; Frise E.; Hodgson A.; George R.A.; Hoskins C.R.; Laverty T.; Muzny D.M.; Nelson C.R.; Pacleb J.M.; Park S.; Pfeiffer B.D.; Richards S.; Sodergren E.J.; RA Svärskas R.; Tabor P.E.; Wan K.; Stapleton M.; Sutton G.G.; Venter C.; Weinstock G.; Scheerer S.E.; Myers E.W.; Gibbs R.A.; Rubin G.M.; RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila melanogaster* euchromatic genome sequence"; RT Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaninker J.S.; Bergman C.M.; Kronmiller B.; Carlson J.; Svirskas R.; Patel S.; Frise E.; Wheeler D.A.; Lewis S.E.; Rubin G.M.; RA Ashburner M.; Celiker S.E.; RT "The transposable elements of the *Drosophila melanogaster* euchromatic genome: a genomics perspective"; RT Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Nasra S.; Crosby M.A.; Mungall C.J.; Matthews B.B.; Campbell K.S.; Hradecky P.; Huang Y.; Kaminker J.S.; Millburn G.H.; Prochnik S.E.; Sutton C.D.; Tupy J.L.; Whitfield E.J.; Bayraktaroglu L.; Berman B.P.; Bettencourt B.R.; Celiker S.E.; de Grey A.D.; Drysdale R.A.; Harris N.L.; Richter J.; Russo S.; Schroeder A.J.; Shu S.Q.; RA Stapleton M.; Yanada C.; Ashburner M.; Gelbart W.M.; Rubin G.M.; RA Lewis S.E.; RT "Annotation of the *Drosophila melanogaster* genome: a systematic review"; RT Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426071; PubMed=12537574;
RA FLYBASE; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RX FLYBASE; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RN [7]
RN SEQUENCE FROM N.A.
RX SPAIN-BERLIN.
RA Stapleton M.; Brookstein P.; Hong L.; Agbayani A.; Carlson J.; Carlson J.; Champe M.; Chavez C.; Dorsett V.; Farfan D.; Friese E.; RA George R.; Gonzalez M.; Guarini B.; Li P.; Liao G.; RA Miranda A.; Mungall C.J.; Nunoo J.; Park J.; Park G.; RA Patel S.; Phouanenavong S.; Wan K.; Yu C.; Lewis S.E.; Rubin G.M.; RA Celinker S.; RT Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [8]
RN FLYBASE; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR FLYBASE; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

RA Rhee J.H.; Kim S.Y.; Chung S.S.; Kim J.J.; Moon Y.H.; Jeong H.; Choi H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted DEC-2002! to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Specifically methylates the cytosine at position 967
 CC (m5C967) of 16S rRNA (By similarity).
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-
 CC homocysteine + rRNA containing C(5)-methylcytosine.
 CC -!- SIMILARITY: Belongs to the methyltransferase superfamily. RsmB/NOP2
 CC subfamily.
 CC EMBL: AP005343; BAC05991.1; -;
 CC InterPro: IPR004573; Fmu_mtfrase.
 CC InterPro: IPR001678; Fmu_NOL1_Nop2P.
 CC InterPro: IPR006027; NusB.
 CC InterPro: IPR006174; NusB_region.
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 DR InterPro: IPR005343; BAC05991.1; -;
 DR InterPro: IPR004573; Fmu_NOL1_Nop2P.
 DR InterPro: IPR001678; Fmu_NusB.
 DR InterPro: IPR006027; NusB.
 DR InterPro: IPR006174; NusB_region.
 DR InterPro: IPR000051; SAM_Bind.
 DR InterPro: IPR000051; NOL1_Nop2_Sun; 1.
 DR Pfam: PF01189; NOL1_Nop2_Sun; 1.
 DR ProDom: PD005242; NusB_dom; 1.
 DR TIGRFAMS: TIGR00563; rsmB; 1.
 DR PROSITE: PS01153; NOL1_Nop2_SUN; 1.
 DR Complete proteome; Methyltransferase; rRNA processing; Transferase.
 SQ DR Sequence: AE016800; AA00533.1; -;
 DR InterPro: IPR004573; Fmu_mtfrase.
 DR InterPro: IPR001678; Fmu_NOL1_Nop2P.
 DR InterPro: IPR006027; NusB.
 DR InterPro: IPR006174; NusB_region.
 DR InterPro: IPR000051; SAM_Bind.
 DR InterPro: IPR000051; NOL1_Nop2_Sun; 1.
 DR Pfam: PF01029; NusB; 1.
 DR ProDom: PD005242; NusB_dom; 1.
 DR TIGRFAMS: TIGR00563; rsmB; 1.
 DR PROSITE: PS01153; NOL1_Nop2_SUN; 1.
 DR Complete proteome; Methyltransferase; rRNA processing; Transferase.
 SQ DR Sequence: D53200063B05CDFC CRC64;
 DR Sequence: 426 AA; 47677 MW; D53200063B05CDFC CRC64;
 DR Sequence: 426 AA; 47677 MW; D53200063B05CDFC CRC64;

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 DR InterPro: IPR005343; BAC05991.1; -;
 DR InterPro: IPR004573; Fmu_NOL1_Nop2P.
 DR InterPro: IPR001678; Fmu_NusB.
 DR InterPro: IPR006027; NusB.
 DR InterPro: IPR006174; NusB_region.
 DR InterPro: IPR000051; SAM_Bind.
 DR Pfam: PF01189; NOL1_Nop2_Sun; 1.
 DR Pfam: PF01029; NusB; 1.
 DR ProDom: PD005242; NusB_dom; 1.
 DR TIGRFAMS: TIGR00563; rsmB; 1.
 DR PROSITE: PS01153; NOL1_Nop2_SUN; 1.
 DR Complete proteome; Methyltransferase; rRNA processing; Transferase.
 SQ DR Sequence: 426 AA; 47677 MW; D53200063B05CDFC CRC64;
 DR Sequence: 426 AA; 47677 MW; D53200063B05CDFC CRC64;

RESULT 31
 RSMB_VIBPA
 JD RSMB_VIBPA STANDARD: PRT; 427 AA.
 AC Q87KQ3;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 RA Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-) (rRNA
 DE (cytosine-C(5)-)methyltransferase) (16S rRNA m5C967
 DE methyltransferase).
 GN Name=rsmB; Synonyms=rsmB; OrderedLocusNames=VP3044;
 DB Vibrioparaheemolyticus
 OC Vibrioparaheemolyticus
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrios; Vibriionales;
 OC Vibrionaceae; Vibrionaceae; vibrio.
 OC NCBI_TaxID=670;
 RN [1]
 RP SEQUENCE FROM N_A.
 RX STRAIN=RIMD 2210633 / Serotype O3:K6;
 RX MEDLINE=22508434; PubMed=12620739;
 RA Makino K., Oshima K., Kurkawa K., Tagomori K., Uda T.,
 RA Iijima Y., Najima M., Nakano M., Yokoyama A., Kubota T., Kimura S.,
 RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
 RA "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
 distinct from that of *V. cholerae*."
 RL Lancet 361:743-749 (2003).
 CC -!- FUNCTION: Specifically methylates the cytosine at position 967
 CC (m5C967) of 16S rRNA. By similarity.
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-
 CC homocysteine + rRNA containing C(5)-methylcytosine.
 CC -!- SIMILARITY: Belongs to the methyltransferase superfamily. RsmB/NOP2
 CC subfamily.
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: AP005083; BAC61307.1; -;
 DR InterPro: IPR004573; Fmu_mtfrase.

RA Rhee J.H.; Kim S.Y.; Chung S.S.; Kim J.J.; Moon Y.H.; Jeong H.; Choi H.E.;
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
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 CC homocysteine + rRNA containing C(5)-methylcytosine.
 CC -!- SIMILARITY: Belongs to the methyltransferase superfamily. RsmB/NOP2
 CC subfamily.
 DR EMBL: AP005083; BAC61307.1; -;
 DR InterPro: IPR004573; Fmu_mtfrase.

DR	InterPro; IPR001678; Fmu_NOL1/Nop2p.	DR	InterPro; IPR0000051; SAM_bind.
DR	InterPro; IPR00627; NusB.	DR	Pfam; PF01189; Nol1_Nop2_Sun; 1.
DR	Pfam; PF000051; SAM_bind.	DR	Pfam; PF01029; NusB; 1.
DR	Pfam; PF01189; Nol1_Nop2_Sun; 1.	DR	PROSITE; PS01153; NOL1 NOP2 SUN; 1.
DR	Pfam; PF0129; NusB; 1.	RW	Complete proteome; Methytransferase; rRNA processing; Transferase.
DR	PROSITE; PS01153; NOL1 NOP2 SUN; 1.	SQ	SEQUENCE 431 AA; 46932 MW; 35C7C763DAB0908B CRC64;
KW	Complete proteome; Methytransferase; rRNA processing; Transferase.	Query Match	30.0%; Score 6; DB 1; Length 431;
SEQUENCE	427 AA; 47835 MW; 653C03351D6B5C CRC64;	Best Local Similarity	100.0%; Pred. No. 1.7e+02;
Matches	6; Conservative 0; Mismatches 0; Indels 0;	Matches	6; Conservative 0; Mismatches 0; Indels 0;
Qy	4 APMWLR 9	Qy	4 APMWLR 9
Db	169 APMWLR 174	Db	167 APMWLR 172
RESULT 32	RESULT 33	RESULT 34	RESULT 34
RSMB_XYLFT	Q7S5V2	Q7S5V2	Q6LLUJ1
ID_RSMB_XYLFT	ID	ID	ID
STANDARD	PRELIMINARY;	PRELIMINARY;	PRELIMINARY;
AC_Q8AFL1	AC	AC	AC
DT_05-JUL-2004 (Rel. 44, Created)	DT	DT	DT
DT_05-JUL-2004 (Rel. 44, Last sequence update)	DT	DT	DT
DT_05-JUL-2004 (Rel. 44, Last annotation update)	DT	DT	DT
DE_Ribosomal RNA small subunit methyltransferase (EC 2.1.1.-) (rRNA (cytosine-C(5)-)methyltransferase) (16S rRNA m5C967 DE_methyltransferase).	DE	DE	DE
GN_Name=rsmb; Synonyms=rmb; OrderedLocusNames=PD1761;	GN	GN	GN
OS_Xylella fastidiosa (strain Temecula / ATCC 700964 / Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.	OS	OS	OS
NCBI_TaxID=183190;	NCBI_TaxID=183190;	SEQUENCE FROM N.A.	SEQUENCE FROM N.A.
RN_[1]	RA_Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Shirniv S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Tanakawa P., Pedersen D., Nelson M., Washburn M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Kothe G.C., Jadd G., Mewes W., Staben C., Marcotte B., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gneire S., Kamal M., Kamysyssels M., Mancelli E., Bielke C., Rudd S., Krishnan D., Kryscioff S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken D., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmann S.A., DeSouza C.C., Glass M.S., Orbach M.J., Berglund J., Voecker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.; "The Genome Sequence of the Filamentous Fungus Neurospora crassa." RT_Nature 0:0-0 (2003).	EMBL/GenBank/DDJB whole genome shotgun (WGS) entry which is preliminary data.	EMBL/GenBank/DDJB whole genome shotgun (WGS) entry which is preliminary data.
RP_SEQUENCE FROM N.A.; PubMed=12533478; MEDLINE=22421331;	RA	RA	RA
RX_Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B., Miyaki C.Y., Furukawa L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H., Takita M.A., Lenos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R., Goldman S.H., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M., Carrer H., Carrasco D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J., Coutinho L.L., Kimura E.T., Ferro B.S., Harakava R., Kurama E.E., Marino R., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M., Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V., da Cunha A.F., Penille R.C., Ferro J.A., Formighieri B.F., Kishi L.T., Leoni S.G., Oliveira A.R., Rosa V.E., Yarai Sasaki F.T., Sena J.A.D., de Souza A.A., Truffi D., Tsuruoka F., Yanai G.M., Zaros L.G., Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C., Kitajima J.P.; "Comparative analyses of the complete genome sequences of Pierce's RT disease and citrus variegated chlorosis strains of Xylella fastidiosa." RT Int J Bacteriol. 185:1018-1026 (2003).	RA	RA	RA
CC_J. FUNCITION: Specifically methylates the cytosine at position 967 (msC967) of 16S rRNA (By similarity).	CC	Query Match	30.0%; Score 6; DB 2; Length 431;
CC_-!_CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-homocysteine + rRNA containing C(5)-methylcytosine.	CC	Best Local Similarity	100.0%; Pred. No. 1.7e+02;
CC_-!_SIMILARITY: Belongs to the methyltransferase superfamily. RsmB/NOP subfamily.	CC	Matches	6; Conservative 0; Mismatches 0; Indels 0;
CC_CThis SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@ish-sib.ch).	CC	Qy	15 LETKFL 20
CC_EMBL; AE012559; AA029595; 1; -	CC	Db	399 LETKFL 404
CC_CThis SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@ish-sib.ch).	CC	RESULT 34	RESULT 34
DR_DR; InterPro; IPR004573; Fmu_Mtfraze.	CC	DR	DR
DR_InterPro; IPR001678; Fmu_NOL1/Nop2p.	CC	DT	DT
DR_InterPro; IPR001601; Methytransferase.	CC	DT	DT
DR_InterPro; IPR00627; NusB.	CC	DE	DE

OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;
OC	Vibrionaceae; Photobacterium.
OX	NCBI TaxID:74109;
RN	
RP	SEQUENCE FROM N.A.
RA	Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., Cestaro A., Malacrida G., Simononati B., Cannata N., Bartlett D., Valle G.;
RA	"Genome analysis of Photobacterium profundum reveals the complexity of high pressure adaptations." Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RT	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RL	EMBL; CR376674; CAG21837.1; -.
DR	InterPro: IPR004573; Fmu_mtfraze.
DR	InterPro: IPR001678; Fmu_NOL1/Nop2p.
DR	InterPro: IPR005027; NusB.
DR	InterPro: IPR006174; NusB region.
DR	InterPro: IPR001639; Sbp_Bac_3.
DR	PFam: PF01189; Nol1_Nop2_Fmu; 1.
DR	TIGRFAMS; TIGR00563; rsmb; 1.
DR	PROSITE; PS001153; NOL1_NOP2_SIN; 1.
DR	PROSITE; PS010339; Sbp_BACTERIAL_3; UNKNOWN_1.
RW	Complete proteome.
SEQUENCE	431 AA; 48054 MW; 1B5D728A0D557688 CRC64;
Qy	Query Match Score 6; DB 2; Length 431; Best Local Similarity 100.0%; Pred. No. 1.7e-02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	4 APNWLR 9 169 APNWLR 174
RESULT 35	
CAG21837	SEQUENCE FROM N.A.
ID	CAG21837 PRELIMINARY; PRT; 431 AA.
AC	CAG21837;
DT	10-MAY-2004 (TRIMBLrel. 27, Created)
DT	10-MAY-2004 (TRIMBLrel. 27, Last sequence update)
DT	10-MAY-2004 (TRIMBLrel. 27, Last annotation update)
DE	Putative Sun protein.
GN	T4095 OR PRPRA3581.
OS	Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;
OC	Vibrionaceae; Photobacterium.
OX	NCBI TaxID:74109;
RN	
RP	SEQUENCE FROM N.A.
RC	STRAIN=ss9;
RA	Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., Cestaro A., Malacrida G., Simononati B., Cannata N., Bartlett D., Valle G.;
RA	"Genome Analysis of Photobacterium profundum reveals the complexity of high pressure adaptations." Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RT	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
RL	EMBL; CR376674; CAG21837.1; -.
DR	Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
SQ	SEQUENCE 431 AA; 48054 MW; 1B5D728A0D557688 CRC64;
Qy	Query Match Score 6; DB 2; Length 431; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	4 APNWLR 9 169 APNWLR 174
RESULT 36	
RSMB_VIBCH	STANDARD; PRT; 434 AA.
ID	R5MB_VIBCH
AC	Q9KVU5;
DT	05-JUL-2004 (Rel. 44, Created)
DT	05-JUL-2004 (Rel. 44, Last sequence update)
DT	01-OCT-2004 (Rel. 45, Last annotation update)
DE	Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-) (rRNA (cytosine-C(5')-methyltransferase) (16S rRNA m5C97-D-methylation).
GN	Name=rsmb; Synonyms=rmb; OrderedLocusNames=VO0044;
OS	Vibrio cholerae; Proteobacteria; Gammaproteobacteria; Vibionales;
OC	Vibrio; Proteobacteria; Gammaproteobacteria; Vibrio.
OX	NCBI_TAXID=666;
RP	[1] SEQUENCE FROM N.A.
RC	STRAIN=El Tor N16961 / Serotype O1, MEDLINE=2040683; PMID=10952301; DOI=10.1038/35020000;
RA	Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L., Brzuskaeva M.D., Vaamondean J.J., Bass S., Qin H., Utterback T.R., Fleischmann R.D., Sellers P., McDonald L.A., Salzberg S.L., White O., Smith H.O., Colwell R.R., Nierman W.C., Mekalanos J.J., Venter J.C., Fraser C.M.;
RA	"DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae." Nature 406:477-483 (2000).
CC	-!- FUNCTION: Specifically methylates the cytosine at position 967 (m5C967) of 16S rRNA (By similarity).
CC	-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-homocysteine + rRNA containing C(5')-methylcytosine.
CC	-!- SIMILARITY: Belongs to the methyltransferase superfamily. RsmB/NOP
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. Its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	CC EMBL; AE004095; AAFF33222.1; -.
CC	CC TIGR; VC0044; -.
CC	CC InterPro; IPR004573; Fmu_mtfraze.
CC	CC InterPro; IPR001678; Fmu_NOL1/Nop2P.
CC	CC InterPro; IPR006027; NusB.
CC	CC PROSITE; PS01153; NOL1 NOP2 SUN; 1.
CC	CC Complete proteome; Methylntransferase; rRNA processing; Transferase.
SQ	Query Match Score 6; DB 1; Length 434; Best Local Similarity 100.0%; Pred. No. 1.7e+02; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	4 APNWLR 9
Db	177 APNWLR 182
RESULT 37	
RSMB_XANAC	STANDARD; PRT; 436 AA.
ID	RSMB_XANAC

AC	RsmB_XANCP	STANDARD;	PRTR;	437 AA.
ID	Q8PG22;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DB	Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-) (rRNA (cytosine-C(5')-methyltransferase). (16S rRNA m5C967)			
DE	Name=rsmB; Synonyms=rsmB, sun; OrderdLocusNames=XAG3799;			
GN	Xanthomonas axonopodis (pv. citri).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;			
OC	Xanthomonadaceae; Xanthomonas.			
NCBI_TaxID	2829;			
[1]	RN			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=306 / ATCC 13902 / XV 101;			
RX	MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;			
RA	da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furian L.R., Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves I.M.C., do Amaral A.M., Bertolini M.C., Camargo J.E.A., Furian L.R., Camarotte G., Cannavan F., Cardozo J., Chambergo P., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Curinso-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., RA			
RA	Ferreirinha E.F., Franco M.C., Greggio C.C., Gruber A., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A., Kashi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Katsuyama A.M., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Medeiros J.J., Miyaki C.Y., Moon D.H., Moreira L.M., Noro M.T.M., Okura V.K., Oliveira V.R., Pereira H.A., Rossi A., Rossini J., Sera J.A.D., Silva C., Spinola L.A.F., Trindade dos Santos M., Tsurita M.A., Tamura R.E., Tezza R.I.D., Setubal J.C., Kitajima J.P.; Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., White F.F.,			
RA	Yamada T., Leite R.P., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Medeiros J.J., Miyaki C.Y., Moon D.H., Moreira L.M., Noro M.T.M., Okura V.K., Oliveira V.R., Pereira H.A., Rossi A., Rossini J., Sera J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., White F.F.,			
RT	Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.			
RT	Nature 417:459-463 (2002).			
CC	-!- FUNCTION: Specifically methylates the cytosine at position 967 (m5C967) of 16S rRNA (By similarity).			
CC	-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + rRNA = S-adenosyl-L-homocysteine + rRNA containing C(5')-methylcytosine.			
CC	-!- SIMILARITY: Belongs to the methyltransferase superfamily. RsmB/NOP CC			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR	EMBL; AE012028; AMM3841_1; -.			
DR	InterPro; IPR004573; Fmu_mtrfrase.			
DR	InterPro; IPR001678; Fmu_NOL1/Nop2P.			
DR	InterPro; IPR006127; NusB.			
DR	InterPro; IPR000051; SAM_Bind.			
DR	Pfam; PF01189; NOL1_Nop2_Sun; 1.			
DR	Pfam; PF01029; NusB; 1.			
DR	ProDom; PD005242; NusB dom; 1.			
DR	TIGRFAMS; TIGR01653; fsmB; 1.			
DR	PROSITE; PS01153; NOL1_Nop2_Sun; 1.			
KW	Complete proteome; Methyltransferase; rRNA processing; Transferase.			
SEQUENCE	436 AA; 47034 MW; 02FF031ED1D04068 CRC64;			
Query Match	30.0% ; Score 6; DB 1; Length 436;			
Best Local Similarity	100.0% ; Pred. No. 1.7e+02;			
Matches	6; Mismatches 0; Indels 0; Gaps 0;			
Qy	4 APMWLR 9			
Db	173 APMWLR 178			
Query Match	30.0% ; Score 6; DB 1; Length 437;			
Best Local Similarity	100.0% ; Pred. No. 1.7e+02;			
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

CC or send an email to license@isib-sib.ch).

CC EMBL; AF006499; AAC9320_1; -.

DR HSSP; P03619; 2DGC.

DR InterPro; IPR004827; TF_bZIP.

DR Pfam; PF00170; bZIP; 1.

DR SMART; SM00338; BRLZ; 1.

DR PROSITE; PS00036; B2ZIP; 1.

DR PROSITE; PS00037; B2ZIP_BASIC; 1.

KW Activator; DNA-binding; Nuclear protein; Transcription regulation.

FT DOMAIN 38 67 Basic motif.

FT DOMAIN 79 107 Leucine-zipper.

SQ SEQUENCE A4A96B12DF5C983 CRC64;

Query Match 30.0%; Score 6; DB 1; Length 583;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RP SEQUENCE FROM N.A.

RC STRAIN=CBS138;

RG GENOMEVERS;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marche C., Neuveglise C., Babour A., Barbe V., Goffard N., Frangeul L., Aigle M., Anthouard V., Bleykasten C., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boistrame A., Boyer J., Catolico L., Conflanier F., de Daruvar A., Desponts L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye P., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszu R., Lemaire M., Oztas S., Ozier-Kalogeropoulos O., Nicaud J.M., Nikolski M., Muller H., Pellenz S., Portier S., Richard G.F., Straub M.L., Suleau A., Swennne D., Tekala F., Wesołowska-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Boilot-Fukuhara M., Thierry A., Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L., "Genome evolution in yeasts.", Nature 430:35-44 (2004).

PL PRINTER; CR380959; CAGE2417.1; ATPase_a/bcentre.

DR InterPro; IPR000194; ATPase_a/bcentre.

DR InterPro; IPR001752; Kinesin_motor.

DR PRINTS; PR00380; KINESINHEAVY.

DR SMART; SM00129; KISC; 1.

DR PROSITE; PS00152; ATPase ALPHA_BETA; UNKNOWN_1.

DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

KW ATP-binding; Microtubule; Motor_protein.

SQ SEQUENCE 7932 MW; 17832DA3A3EA98FE CRC64;

Query Match 30.0%; Score 6; DB 2; Length 672;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 MLETKF 19

DB 612 MLETKF 617

RESULT 45

Q6FK03 PRELIMINARY; PRT; 672 AA.

ID Q6FK03 ; AC Q6FK03 ; DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE similar to sp P28743 Saccharomyces cerevisiae YPL155c KIP2 kinesin-related protein

GN ORFNames=CGLM02189g;

Candida glabrata (yeast) (Torulopsis glabrata); Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces; Saccharomycetales; mitosporic Saccharomycetales; Candida.

NCBI_TaxID=5478;

RN [1]

RP SEQUENCE FROM N.A.

RC

RG

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marche C., Neuveglise C., Babour A., Barbe V., Goffard N., Frangeul L., Aigle M., Anthouard V., Bleykasten C., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boistrame A., Boyer J., Catolico L., Conflanier F., de Daruvar A., Desponts L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye P., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszu R., Lemaire M., Oztas S., Ozier-Kalogeropoulos O., Nicaud J.M., Nikolski M., Muller H., Pellenz S., Portier S., Richard G.F., Straub M.L., Suleau A., Swennne D., Tekala F., Wesołowska-Louvel M., Westhof E., Wirth B., Zeniou-Meyer M., Zivanovic I., Boilot-Fukuhara M., Thierry A., Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L., "Genome evolution in yeasts.", Nature 430:35-44 (2004).

PL PRINTER; CR380959; CAGE2417.1; ATPase_a/bcentre.

DR InterPro; IPR000194; ATPase_a/bcentre.

DR InterPro; IPR001752; Kinesin_motor.

DR PRINTS; PR00380; KINESINHEAVY.

DR SMART; SM00129; KISC; 1.

DR PROSITE; PS00152; ATPase ALPHA_BETA; UNKNOWN_1.

DR PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.

KW ATP-binding; Microtubule; Motor_protein.

SQ SEQUENCE 7932 MW; 17832DA3A3EA98FE CRC64;

Query Match 30.0%; Score 6; DB 2; Length 672;

Best Local Similarity 100.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 MLETKF 19

DB 612 MLETKF 617

RESULT 46

Q7P394 PRELIMINARY; PRT; 772 AA.

ID Q7P394 ; AC Q7P394 ; DT 01-MAR-2004 (TREMBLrel. 26, Created)

DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Hypothetical membrane spanning protein.

GN Name=TNV217;

OS Fusobacterium nucleatum subsp. vincentii ATCC 49226.

OC Fusobacteria; Fusobacteriales; Fusobacteriaceae;

OC

RA Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhalova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyripides N.;

RA

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 49226;

RA

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC !- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; AABP0100003; EAA25145.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 772 AA; 90058 MW; 4B861956C1F51058 CRC64;
 Query Match Score 6; DB 2; Length 772;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 LETKFL 20
 Db 300 LETKFL 305

RESULT 47
 Q8RGCGO PRELIMINARY; PRT; 772 AA.
 ID Q8RGCGO ;
 AC Q8RGCGO ;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-OCT-2002 (TrEMBLrel. 21, Last annotation update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FN0384.
 GN OS Fusobacterium nucleatum (subsp. nucleatum) .
 OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
 OC Fusobacterium
 OX NCBI_TaxID=76855;
 RN [1]
 RP SEQUENCE FROM N.A.; STRAIN=ATCC 25586;
 RX Kapatral V, Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Greshkin G., Zhu L.,
 RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fonstein N., Kyriides N.C., Overbeek R.,
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 nucleatum strain ATCC 25586".
 RL J. Bacteriol.184:2005-2018 (2002).
 DR EMBL; A010549; AAL94587.1; -.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 772 AA; 90123 MW; 9B3A35DF/FFCB213 CRC64;
 Query Match Score 6; DB 2; Length 772;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 15 LETKFL 20
 Db 300 LETKFL 305

RESULT 48
 Q93325 PRELIMINARY; PRT; 793 AA.
 ID Q93325 ;
 AC Q93325 ;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein C33G3.1a (DYC-1 protein) (Fragment).
 GN Name=C33G3.1a; Synonyms=dyc-1;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.; STRAIN=Bristol N2;
 RC Gajadhar S.;
 RX Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 [3]

RESULT 49
 Q8STF6 PRELIMINARY; PRT; 887 AA.
 ID Q8STF6 ;
 AC Q8STF6 ;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-OCT-2004 (TrEMBLrel. 21, Last sequence update)
 DE Hypothetical protein C33G3.1b.
 GN Name=C33G3.1b;
 OS Caenorhabditis elegans.
 OC Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.; STRAIN=Bristol N2;
 RC Gajadhar S.;
 RX Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 [3]

RESULT 50
 Q9069613 PRELIMINARY; PRT; 9851916;
 ID Q9069613 ;
 AC Q9069613 ;
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein C33G3.1a (DYC-1 protein) (Fragment).
 GN Name=C33G3.1a; Synonyms=dyc-1;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peioderinae; Caenorhabditis.
 NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.; STRAIN=Bristol N2;
 RC Mathew L.;
 RX Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 [3]

DR	EMBL; Z72501; CAD30431.1; JOINED.	ID	Q8A180	PRELIMINARY;	PRT;	1345 AA.
DR	EMBL; Z78500; CAD30431.1; -.	AC	Q8A180;			
DR	INTACT; Q83TP6; -.	DT	01-JUN-2003	(TREMBLref)	24;	Created
DR	WormPep; C3G3.1b; CB30500.	DT	01-JUN-2003	(TREMBLref)	24;	Last sequence update
DR	InterPro; IPR011036; PH related.	DT	01-OCT-2003	(TREMBLref)	25;	Last annotation update
DR	InterPro; IPR0060320; PTB_PID.	DE	Two-component system sensor kinase/response regulator			
DR	PFam; PF00640; PID; 1.	DE	hybrid ('one-component system').			
DR	SMART; SMM00462; PTB; 1.	GN	OrderdLocusNames=BP3786;			
DR	PROSITE; PS001179; PTD; 1.	OS	Bacteroides thetaiotaomicron.			
KW	Hypothetical protein.	OC	Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;			
SEQUENCE	887 AA; 99567 MW; 4479D811513A9CAS CRC64;	OC	Bacteroidaceae; Bacteroides.			
SQ	NCBI_TaxID=818;	OX	NCBI_TaxID=818;			
Query Match	30.0%; Score 6; DB 2; Length 887;	RN	[1]			
Best Local Similarity	100.0%; Pred. No. 3.2e+02;	SEQUENCE FROM N.A.				
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	STRAIN=VPI-5482 / ATCC 29148;	STRAIN=VPI-5482;				
Qy	13 QMLETK 18	RP	PubMed=22550858;			
Db	497 QMLETK 502	RX	HSSP; AE016942; AAC078891.1; -.			
RESULT 50		DR	DR			
QYVYV13	PRELIMINARY;	DR	DR			
ID	Q7YYV13;	DR	DR			
AC	Q7YYV13;	DR	DR			
DT	01-OCT-2003 (TREMBLref) 25; Created	GO	GO; GO:0005622; C:intracellular; IEA.			
DT	01-OCT-2003 (TREMBLref) 25; Last sequence update	DR	DR			
DT	01-MAR-2004 (TREMBLref) 26; Last annotation update	GO	GO; GO:000524; F:ATP binding; IEA.			
DE	Protein kinase, putative.	DR	DR			
GN	ORFNames=tp9227_2.4200;	GO	GO; GO:0003700; F:transcription factor activity; IEA.			
OS	Trypanosoma brucei.	DR	GO; GO:0000156; F:two-component response regulator activity; IEA.			
OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.	DR	GO; GO:0000155; F:two-component sensor molecule activity; IEA.			
OX	NCBI_TaxID=691;	DR	DR			
RN		DR	DR			
RP	SEQUENCE FROM N.A.	DR	DR			
RX	MEDLINE=22789168; PubMed=12907728;	DR	DR			
RA	El-Sayed N.M.A., Ghedin E., Song J., Macleod A., Bringaud F.,	DR	DR			
RA	Wanless D., Peterson J., Taylor S., Tweedie A.,	DR	DR			
RA	Larkin C., Khalek H.G., Lin X., Mason T., Hannick L., Caler E.,	DR	DR			
RA	Biteau N., Bartholomeeu D., Simpson A.J., Kaul S., Zhao H., Pai G.,	DR	DR			
RA	Blandin G., Utterback T., Haas B., Koo H.L., Umayan L., Suh B.,	DR	DR			
RA	Van Aken S., Gerrard C., Leech V., Qi R., Zhou S., Schwartz D., Feldblum T.,	DR	DR			
RA	Salzberg S., Tait A., Turner M.R., Ullu E., White O., Melville S.,	DR	DR			
RA	Adams M.D., Fraser C.M., Donegan J.E.;	DR	DR			
RT	"The sequence and analysis of <i>Trypanosoma brucei</i> chromosome II."	DR	DR			
RL	Nucleic Acids Res. 31:4855-4863(2003).	DR	DR			
CC	-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.	DR	DR			
DR	EMBL; AE017169; AAQ15677.1; -.	PRINTS; PR00032; HTBARAC.				
DR	GO; GO:0005524; F:ATP binding; IEA.	PRODOM; PD000039; HTBARAC.				
DR	GO; GO:004674; P:protein serine/threonine kinase activity; IEA.	SMART; SM00387; HTAPase C; 1.				
DR	GO; GO:0016740; P:protein kinase; 1.	PFAM; PF00512; HTSKA; 1.				
DR	PROSITE; PS00001; Prot kinase; 1.	PFAM; PF00165; HTH_AracC; 2.				
DR	PROSITE; PS00011; PROTEIN KINASE ATP; UNKNOWN 1.	PFAM; PF07494; Reg_prop; 11.				
DR	PROSITE; PS00010; PROTEIN KINASE DOM; 1.	PFAM; PF00072; Response_reg; 1.				
DR	PROSITE; PS00010; PROTEIN_KINASE_ST; 1.	PFAM; PF07495; Y_V_Y; 1-				
KW	ATP-binding Kinase; Serine/threonine-protein kinase; Transferase.	PRINTS; PR00032; HTBARAC.				
SEQUENCE	1037 AA; 113326 MW; A87B8C4422745274 CRC64;	PRODOM; PS000039; HTBARAC.				
Qy	11 VCOMLE 16	SMART; SM00448; REC/-1.				
Db	85 VCOMLE 90	PROSITE; PS00109; HIS_KIN; 1.				
Query Match	30.0%; Score 6; DB 2; Length 1037;	DR	PROSITE; PS01124; HTH_ARAC_FAMILY 2; 1.			
Best Local Similarity	100.0%; Pred. No. 3.7e+02;	DR	PROSITE; PS00110; RESPONSE_REGULATORY; 1.			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	Complete proteome; DNA-binding; Kinase; Phosphorylation				
SQ	SEQUENCE 1345 AA; 155269 MW; 7227BDDA9C7FADAB CRC64;	KW	Sensory transduction; Transcription regulation; Transferase.			
Query Match	30.0%; Score 6; DB 2; Length 1345;	DR	PROSITE; PS00032; HTBARAC.			
Best Local Similarity	100.0%; Pred. No. 4.6e+02;	DR	PROSITE; PS00109; HIS_KIN; 1.			
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	PROSITE; PS00110; RESPONSE_REGULATORY; 1.				
Qy	11 VCOMLE 16	DR	Complete proteome; DNA-binding; Kinase; Phosphorylation			
Db	85 VCOMLE 90	KW	Sensory transduction; Transcription regulation; Transferase.			
RESULT 52		DR	PROSITE; PS00032; HTBARAC.			
Q9UPZ6	PRELIMINARY;	DR	PROSITE; PS00109; HIS_KIN; 1.			
ID	Q9UPZ6;	DR	PROSITE; PS00110; RESPONSE_REGULATORY; 1.			
AC	Q9UPZ6;	DR	Complete proteome; DNA-binding; Kinase; Phosphorylation			
DT	01-MAY-2000 (TREMBLref). 13, Created)	KW	Sensory transduction; Transcription regulation; Transferase.			
RESULT 51		DR	PROSITE; PS00032; HTBARAC.			
Q8A180	PRELIMINARY;	DR	PROSITE; PS00109; HIS_KIN; 1.			

Q	A	Sequence	Query Match	Best Local Similarity	Score	Pred.	Length	Indels	Gaps	Matches	Conservative	Mismatches	Index	Gaps	
<i>WormPep; F54B.1; CE17885. Hypothetical protein.</i>															
SEQUENCE 3396 AA; 391879 MW; 337F20A3A9BD2CE7 CRC64;															
Y	b	13 QMLETK 18	Q83SX5	PRELIMINARY;	PRT;	23 AA.	RESULT 56	Q80KE7	PRELIMINARY;	PRT;	28 AA.				
		1962 QMLETK 1967	Q83SX5	01-TUN-2003 (TREMBrel. 24, Created)	AC	Q80KE7;		AC	01-JUN-2003 (TREMBrel. 24, Created)	DT	01-JUN-2003 (TREMBrel. 24, Last sequence update)				
			Q83SX5	01-JUN-2003 (TREMBrel. 24, Last sequence update)	AC	Q80KE7;		AC	01-JUN-2003 (TREMBrel. 24, Last sequence update)	DT	01-JUN-2003 (TREMBrel. 24, Last annotation update)				
				Hypothetical protein.											
				OrderedLocusNames=2947;											
				Salmonella typhi.											
				Bacteriia; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonellae.											
				[1] _											
				SEQUENCE FROM N.A. NCBI_TaxID=601;											
				STRAIN=TCC2 / ATCC 700931;											
				MEMLINE=225311267; PubMed=12644504;											
				Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.T.,											
				Burland V., Kodoyanni V., Schwartz D.C., Blattner F.R.;											
				"Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2 and CT18.";											
				J. Bacteriol. 185:2330-2337 (2003).											
				EMBL; AED16844; AED0705001; -.											
				Hypothetical protein.											
				SEQUENCE 23 AA; 2797 MW;											
				9EEB0FCB88CB36AA CRC64;											
				SEQUENCE 23 AA;											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											
				Best Local Similarity 100.0%; Pred. No. 1.7e+02;											
				Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;											
				11 VCQML 15											
				16 VCQML 20											
				Query Match Score 5%; DB 2; Length 23;											

ID	Q80KF0;	PRELIMINARY;	PRT;	28 AA.	OX NCBI_TaxID=11292;
AC	Q80KF0;				RN [1] SEQUENCE FROM N.A.
DT	01-JUN-2003	(T)RMBLrel.	24	Created	RP MEDLINE=22541850; PubMed=12655080;
DT	01-JUN-2003	(T)RMBLrel.	24	Last sequence update	RX Paez A., Nunez C., Garcia C., Boselli J.;
DT	01-JUN-2003	(T)RMBLrel.	24	Last annotation update	RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."
DE	L protein (Fragment).				RT
OS	Rabies virus.				RT
OC	Virus; ssRNA negative-strand viruses; Mononegavirales;				RL J. Gen. Virol. 84:795-802(2003).
OC	Rhabdoviridae; Lyssavirus.				DR EMBL; AY192389; AAO45864.1; -.
OX	NCBI_TaxID=11292;				FT NON-TER 28 28
RN	[1]				SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;
RP					
SEQUENCE FROM N.A.					
RX	MEDLINE=22541850; PubMed=12655080;				
RA	Paez A., Nunez C., Garcia C., Boselli J.;				
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."				
RT	J. Gen. Virol. 84:795-802(2003).				
RT	EMBL; AY192392; AAO45867.1; -.				
RL					
DR					
FT	NON-TER 28				
SQ	SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;				
RESULT 61					
Q80KF2					
ID	Q80KF2	PRELIMINARY;	PRT;	28 AA.	
AC	Q80KF2;				
DT	01-JUN-2003	(T)RMBLrel.	24	Created	RN [1] SEQUENCE FROM N.A.
DT	01-JUN-2003	(T)RMBLrel.	24	Last sequence update	RP MEDLINE=22541850; PubMed=12655080;
DT	01-JUN-2003	(T)RMBLrel.	24	Last annotation update	RA Paez A., Nunez C., Garcia C., Boselli J.;
DE	L protein (Fragment).				RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."
OS	Rabies virus.				RT
OC	Virus; ssRNA negative-strand viruses; Mononegavirales;				RL J. Gen. Virol. 84:795-802(2003).
OC	Rhabdoviridae; Lyssavirus.				DR EMBL; AY192389; AAO45863.1; -.
OX	NCBI_TaxID=11292;				FT NON-TER 28 28
RN	[1]				SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;
RP					
SEQUENCE FROM N.A.					
RX	MEDLINE=22541850; PubMed=12655080;				
RA	Paez A., Nunez C., Garcia C., Boselli J.;				
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."				
RT	J. Gen. Virol. 84:795-802(2003).				
RT	EMBL; AY192390; AAO45865.1; -.				
RL					
FT	NON-TER 28				
SQ	SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;				
RESULT 62					
Q80KF3					
ID	Q80KF3	PRELIMINARY;	PRT;	28 AA.	
AC	Q80KF3;				
DT	01-JUN-2003	(T)RMBLrel.	24	Created	RN [1] SEQUENCE FROM N.A.
DT	01-JUN-2003	(T)RMBLrel.	24	Last sequence update	RP MEDLINE=22541850; PubMed=12655080;
DT	01-JUN-2003	(T)RMBLrel.	24	Last annotation update	RA Paez A., Nunez C., Garcia C., Boselli J.;
DE	L protein (Fragment).				RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."
OS	Rabies virus.				RT
OC	Virus; ssRNA negative-strand viruses; Mononegavirales;				RL J. Gen. Virol. 84:795-802(2003).
OC	Rhabdoviridae; Lyssavirus.				DR EMBL; AY192387; AAO45862.1; -.
OX	NCBI_TaxID=11292;				
RN	[1]				
RP					
SEQUENCE FROM N.A.					
RX	MEDLINE=22541850; PubMed=12655080;				
RA	Paez A., Nunez C., Garcia C., Boselli J.;				
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."				
RT	J. Gen. Virol. 84:795-802(2003).				
RT	EMBL; AY192391; AAO45866.1; -.				
RL					
FT	NON-TER 28				
SQ	SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;				
RESULT 64					
Q80KF5					
ID	Q80KF5	PRELIMINARY;	PRT;	28 AA.	
AC	Q80KF5;				
DT	01-JUN-2003	(T)RMBLrel.	24	Created	RN [1] SEQUENCE FROM N.A.
DT	01-JUN-2003	(T)RMBLrel.	24	Last sequence update	RP MEDLINE=22541850; PubMed=12655080;
DT	01-JUN-2003	(T)RMBLrel.	24	Last annotation update	RA Paez A., Nunez C., Garcia C., Boselli J.;
DE	L protein (Fragment).				RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."
OS	Rabies virus.				RT
OC	Virus; ssRNA negative-strand viruses; Mononegavirales;				RL J. Gen. Virol. 84:795-802(2003).
OC	Rhabdoviridae; Lyssavirus.				DR EMBL; AY192387; AAO45862.1; -.
OX	NCBI_TaxID=11292;				
RN	[1]				
RP					
SEQUENCE FROM N.A.					
RX	MEDLINE=22541850; PubMed=12655080;				
RA	Paez A., Nunez C., Garcia C., Boselli J.;				
RT	"Molecular epidemiology of rabies epizootics in Colombia: evidence for human and dog rabies associated with bats."				
RT	J. Gen. Virol. 84:795-802(2003).				
RT	EMBL; AY192392; AAO45867.1; -.				
RL					
FT	NON-TER 28				
SQ	SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;				

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE L protein (Fragment).
 OS Rabies virus.
 OC Rhabdoviridae; *Lyssavirus*; Mononegavirales;
 NCBI_TaxID=11292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A., Nunez C., Garcia C., Boselli J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192380; AA045854.1; -.
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;

Query Match Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 21 PRGAP 25

RESULT 70
 ID Q80KG3 PRELIMINARY; PRT; 28 AA.
 AC Q80KG3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DB L protein (Fragment).
 OS Rabies virus.
 OC Rhabdoviridae; *Lyssavirus*; Mononegavirales;
 NCBI_TaxID=11292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A., Nunez C., Garcia C., Boselli J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192379; AA045854.1; -.
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AAC3C6A CRC64;

Query Match Score 5; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
 Db 21 PRGAP 25

RESULT 71
 ID Q80KG4 PRELIMINARY; PRT; 28 AA.
 AC Q80KG4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DB L protein (Fragment).
 OS Rabies virus.
 OC Rhabdoviridae; *Lyssavirus*; Mononegavirales;
 NCBI_TaxID=11292;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22541850; PubMed=12655080;
 RA Paez A., Nunez C., Garcia C., Boselli J.;
 RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
 human and dog rabies associated with bats.";
 RL J. Gen. Virol. 84:795-802(2003).
 DR EMBL; AY192374; AA045849.1; -.
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 2998 MW; 2E3147A9AAC3CCA CRC64;

Query Match Score 5; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 74

Q80KG9 PRELIMINARY;
ID Q80KG9;
AC Q80KG9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssaviruses.
OX NCBI_TaxID=11292;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Boshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL: AY192373; AAO45848.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 21 PRGAP 25

RESULT 75

Q80KHO PRELIMINARY;
ID Q80KHO;
AC Q80KHO;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE L protein (Fragment).
OS Rabies virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Lyssaviruses.
OX NCBI_TaxID=11292;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22541850; PubMed=12655080;
RA Paez A., Nunez C., Garcia C., Bosshell J.;
RT "Molecular epidemiology of rabies epizootics in Colombia: evidence for
RT human and dog rabies associated with bats.";
RL J. Gen. Virol. 84:795-802(2003).
DR EMBL: AY192372; AAO45847.1; -.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3010 MW; 2E3637A9AACAA3C6A CRC64;

Query Match 25.0%; Score 5; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PRGAP 5
Db 21 PRGAP 25

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RESULT 1		RESULT 2		RESULT 3	
AAAB11672	AAB11672 standard; protein; 106 AA.	AAV76621	AAY76621 standard; protein; 147 AA.	Query Match	Score 6 ; DB 3 ; Length 106 ; Best Local Similarity 100.0% ; Pred. No. 80 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	XX	XX	XX	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
AC	AAC	AC	AAY76621 ;	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	XX	XX	XX	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
DT	23-OCT-2000 (first entry)	DT	10-APR-2000 (first entry)	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	XX	XX	XX	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
DE	A. vitis hypersensitive response elicitor protein, SEQ ID NO:59.	DE	Human ovarian tumor EST fragment encoded protein lii7.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	Hypersensitive response elicitor protein; HR; disease resistance; insecticide; fungicide; antiviral; bactericide; growth enhancer; stress resistance; transgenic plant.	XX	Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	Agrobacterium vitis.	XX	XX	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
OS	PN	PN	PN	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	W020028056-A2.	XX	XX	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	18-MAY-2000.	XX	XX	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
IPD	05-NOV-1999 ; 99W0-US026079.	IPF	09-APR-1998 ; 98DE-01017557.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	XX	XX	XX	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
IPR	06-NOV-1998 ; 98US-0107387P.	IPR	09-APR-1998 ; 98DE-01017557.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	(CORR) CORNELL RES FOUND INC.	PA	(META-) METAGEN GES GENOMFORSCHUNG MBH.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	Burr TJ, Herlache TC, Zhang H;	PI	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	WPI; 2000-376567/32.	DR	WPI; 1999-591920/51.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
DR	N-PSDB; AAA61517.	DR	N-PSDB; AAZ74972.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	New protein from Agrobacterium vitis, useful e.g. for imparting resistance to disease or stress to plants, is involved in production of a hypersensitive response.	XX	New nucleic acid sequences expressed in ovarian, and some other, cancer tissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
PS	Claim 3; Page 131; 157pp; English.	PS	Claim 25; Page 222; 310pp; German.	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	Sequences AAB11630-B11688 represent proteins from Agrobacterium vitis which elicit a hypersensitivity response (HR) in a plant. The invention also relates to nucleotide sequences (AA61501-AA61524) encoding the A. vitis HR elicitor proteins. The HR is a rapid, localised necrosis that is associated with the active defence of plants against many pathogens, and occurs when a pathogenic organism interacts with a nonhost plant (i.e. one in which intracellular bacterial growth and disease development do not occur). Like other HR elicitors, the A. vitis elicitor functions in non-host plants by causing a rapid hypersensitive response that results in walling off and killing of the pathogen. On grape plants, the A. vitis elicitor induces a restricted necrosis of tissues, resulting in the death of plant cells and induction of pathogen resistance. A. vitis HR elicitor proteins, in non-infectious form, are used to treat plants or their seeds to impart resistance to disease, such as those caused by fungi, bacteria or viruses; and to enhance growth, e.g., to increase yield or to provide earlier germination or maturation. The proteins can also be used to control insects, to impart resistance to environmental stresses, e.g., cold, and to improve nutritional value, e.g., altered oil content. The same effects can be produced by producing transgenic plants or seeds by incorporation of DNA that encodes A. vitis HR elicitor proteins. Use of A. vitis HR elicitor proteins, or nucleic acids encoding them, may allow control of previously untreatable diseases; provide systemic treatment and eliminate the need for biological control agents or polluting chemicals.	CC	This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy; (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (C) are identified by assembling ESTs (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AAY76505-Y76638 represent protein fragments encoded by the human ovarian tumor cDNA library derived EST fragments represented in AAZ77450-Z77572	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
PS	Sequence 147 AA;	SQ	Sequence 147 AA;	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	Sequence 106 AA;	DB	27 PRGAPM 32	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
XX	Sequence 106 AA;	DB	27 PRGAPM 32	Query Match	Score 6 ; DB 2 ; Length 147 ; Best Local Similarity 100.0% ; Pred. No. 1e+02 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

ABO62427
 ID ABO62427 standard; protein; 169 AA.
 XX
 AC ABO62427;
 XX
 DT 29-JUL-2004 (first entry)
 XX Klebsiella pneumoniae polypeptide seqid 8944.
 DE Recombinant expression vector; transcription regulatory element;
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
 XX
 OS Klebsiella pneumoniae.
 XX
 PN US6610836-B1.
 XX
 PD 26-AUG-2003.
 XX
 PP 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton GL, Osborne M;
 XX
 DR 2003-895346/82.
 DR N-PSDB; ACH95978.
 XX
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 preparing a vaccine composition against Klebsiella pneumoniae.
 XX
 Disclosure: SEQ ID NO 8944; 932PP; English.
 XX
 The invention describes a new isolated nucleic acid encoding a Klebsiella
 pneumoniae polypeptide. Also described are: a recombinant expression
 vector comprising the nucleic acid, operably linked to a transcription
 regulatory element; and a cell comprising the recombinant expression
 vector. The nucleic acid is useful for preparing a vaccine composition
 against Klebsiella pneumoniae. This is the amino acid sequence of a
 Klebsiella pneumoniae polypeptide of the invention
 XX
 Sequence 169 AA;
 SQ Score 30.0%; Score 6; DB 7; Length 169;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 GAPMWL 8
 Db 90 GAPMWL 95

RESULT 4
 ABP42001
 ID ABP42001 standard; protein; 285 AA.
 XX
 AC ABP42001;
 XX
 DT 22-AUG-2002 (first entry)
 XX Human ovarian antigen HTEL95, SBQ ID NO:3133.
 DE Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.

XX Homo sapiens.
 CS XX
 PN WO200200577-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rossen CA;
 XX
 DR WPI; 2002-147878/19.
 DR N-PSDB; ABQ55078.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 useful in the prevention, treatment and diagnosis of cancer (e.g., ovarian
 cancer), immune disorders, cardiovascular disorders and neurological
 diseases.

XX
 PS Claim 11; SEQ ID NO 3133; 2922PP; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 encompasses polypeptides 90% identical and polynucleotides 95% identical
 to the sequences of the invention. The invention additionally relates to
 recombinant vectors and host cells comprising human ovarian antigen
 polynucleotides, antibodies against human ovarian antigens, and the use
 of ovarian antigen polynucleotides and polypeptides in diagnosing,
 treating, prophesing or preventing various ovary and/or breast-related
 disorders. Such conditions include ovarian cancer and breast cancer, and
 metastatic tumours of ovary or breast origin, reproductive system
 disorders (e.g., infertility, disorders of pregnancy, anovulation,
 polycystic ovary syndrome, ovarian cysts, and dysmenorrhoeal, endocrine
 disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 vaginitis), immune disorders (e.g., congenital and acquired
 immunodeficiencies, autoimmune oophritis, systemic lupus erythematosus),
 blood-related disorders (e.g., anaemia), cardiovascular disorders,
 respiratory disorders, neurological disorders, gastrointestinal disorders
 and urinary system disorders. Ovarian antigen polypeptides and
 polynucleotides may also be used in screening for compounds which
 modulate ovarian antigen expression or activity. The polynucleotides may
 further be used for gene therapy, chromosome mapping, in the
 identification of individuals and in forensic analysis, and the
 polypeptides may be used as food additives or to prepare antibiotics
 useful in disease diagnosis, drug targeting and phenotyping. The present
 sequence represents a human ovarian antigen of the invention. Note: The
 sequence data for this patent did not form part of the printed
 specification, but was obtained in electronic format directly from WIPO
 at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

XX
 SQ Sequence 285 AA;

Query Match 30.0%; Score 6; DB 5; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LETKFL 20
 Db 178 LETKFL 183

RESULT 5
 ABP60658
 ID ABP60658 standard; protein; 315 AA.
 XX
 AC ABP60658;
 XX
 DT 26-MAR-2002 (first entry)

